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Jan 27 14:04:07 2003
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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                   Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  number of hits satisfying chosen parameters:
       SPTREMBL_21:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_volent:*
12: sp_virus:*
13: sp_vertebrate
14: sp_unclassifi
15: sp_bacteriap::
16: sp_bacteriap:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        January 24, 2003, 19:40:10 ; Search time 35 Seconds (without alignments) 2095.794 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-675-509-4
1802
1 MSTQPKTLTVGLFPYLPSWN......CVDFANKEVKNCAGVLRPFL 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       671580 segs, 206047115 residues
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Gapop 10.0 , Gapext 0.5
sp_organelle:*
sp_phage:*
sp_plant:*
sp_virus:*
sp_vertebrate:*
sp_vertebrate:*
sp_rvirus:*
sp_rvirus:*
sp_archeap:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                              sp_invertebrate:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	, 12	11	10	9	8	7	6	ű	4	ω	2	,	Result No.
106.5	106.5	107	108	108.5	109	110.5	110.5	111	111.5	111.5	112.5	114.5	115	116	118.5	Score
5.9	5.9	5.9	6.0	6.0	6.0	6.1	6.1	6.2	6.2	6.2	6.2	6.4	6.4	6.4	6.6	Query
1033	1007	2081	528	998	448	912	718	417	1414	613	1360	1431	286	1248	345	Query Match Length
10	9	17	თ	v	10	_	10	٠.	17	17	v	v	N	10	16	DB
Q9CAA7	Q9F4J3	Q9HJ37	Q20730	044800	024399	070410	Q94JF5	Q8RBL7	Q8TH79	Q97YF0	015807	Q9XYH6	Q9RLV6	Q9SAJ2	Q8RD78	ij
Q9caa7 arabidopsis	Q9f4j3 streptococc	Q9hj37 thermoplasm	Q20730 caenorhabdi	O44800 caenorhabdi	O24399 triticum ae	_	Q94jf5 oryza sativ	Q8rb17 thermoanaer	Q8th79 methanosarc	Q97yf0 sulfolobus	O15807 cryptospori	Q9xyh6 cryptospori	Q9rlv6 lactococcus	Q9saj2 arabidopsis	Q8rd78 thermoanaer	Description

15 10	44 10	43 10	42 10	41	40 10		38	37	36	35		33 10	32 10	31 10				27 10								19		17 10
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5.6	5.6	5. 6	5.6	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7					ა. 8									5.9
767	728	703	505	578	704	598	2701	1857	738	637	286	4643	1733	692	689	2806	2462	628	503			602	358	1220	1054	545	2819	1166
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Q94543	Q9M9S4	Q93MA0	Q93335	Q9SDM7	031399	Q9L746	Q8WN96	Q8TGC5	Q9AQF4	Q92DW5	Q9CIN5	Q9VW71	QBTTS9	Q97YM6	Q8RSZ0	Q8RI19	Q8RGZ3	Q9PQ47	Q97XR3	Q9I943	050698	Q8RBX6	Q928M1	Q9P3A8	Q9PR50	Q9V283	Q98QP8	Q8V7K1
Q94543 drosophila	Q9m9s4 arabidopsis	Q93ma0 clostridium	Q93335 caenorhabdi	Q9sdm7 glycine max	O31399 bacillus su	Q91746 haemophilus		Q8tgc5 aspergillus	Q9aqf4 clostridium	Q92dw5 listeria in	Q9cin5 lactococcus	Q9vw71 drosophila	Q8tts9 methanosarc	Q97ym6 sulfolobus	Q8rsz0 pseudomonas	Q8ri19 fusobacteri	Q8rgz3 fusobacteri	Q9pq47 ureaplasma	Q97xr3 sulfolobus	Q9i943 carassius a	O50698 borrelia bu	Q8rbx6 thermoanaer	Q928ml listeria in	m	0		Q98qp8 mycoplasma	Q8v7k1 chlorella v

ALIGNMENTS

Qy 1	Db 1	Ş	망	Qy	Best Lo Matches			C E									RN [1]									DT 01		1D 08	RESULT
128 GTQQASSLLELAQKVG-	:	71FLPYLVS	41 EGGKSVKLDH	21 ENGNEVKLIN	cal Simi 73;	Match	345	EMBL; AE012990; AAM23469.1; Complete proteome.	3101000	"A complete sequence of Genome Res. 12:689-700()	Tan H., Chen R.,		o Q., Tian Y.,	m	34T /	SEQUENCE FROM N.A.		NCBI TaxID=119072;	Thermoanaerobacteriales;	Bacteria; Firmicutes;	Thermoanaerobacter	SPOIID OR TTE0168		_	_	-2002 (•	OBRD78 PRE	ם
1 1 1 1	-	FLPYLVSLGGVKSLDESLVRGVTGDLHSFVSSASVNGSVYGFPQYLCSNFLLSSPN	EGGKSVKLDKLPSYEVIRVFITNQNKIEEMQLEDYVKGVVAAEMPAEFEIEALKAQAVAA	ENGNEVKLINLIK-DVLPTQVSGYN-IEYTEFDCYSDASLQS-LPDVFSTDSI-	21.3%; vative		AA; 38528 MW;			T.	; ~	Хи Y.,	μ. Σ.	6; PubMed=11997336;	JCM11007;	ī.A.)72;		89	ter tengcongensis	•	_		TrEMBLrel. 21.	TrEMBLrel. 21,		PRELIMINARY;	
YEQI	-KGCDLHEGVD	RGVTGDLHSFVSS	NONKIEEMQLEDY	GYN-IEYTEFDCY	60; Mismatches	118.		.•		tengcongensis	Yang	Huang L	n 2.,	997336;					Thermoanaerobacteriaceae;	Bacillus/Clostridium group;	ensis.		related proteins.		Last sequence	Created)		PRT; 345	
VYPDVASSS		SASVNGSVYGFP	VKGVVAAEMPAE	SDASLQS-LPDV	118;	; DB 16;	B75DD6A0FB89AC57 CRC64;			genome.";		Dong	Hu S., Dong W						••				•		e update)			AA.	
-VYPDVASSSSFTVFGLYQQLLQ	VCTDF	QYLCSNFLLSSE	FEIEALKAQAVA	FSTDSI	Indels 91;	Length 345;	4;					Y., Ling	., Yang J						Thermoanaerobacter.	Clostridia;									
Ø 169	FE 129	N 127	VA 100	70	Gaps 17;							Ľ.,							acter.										

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A VYSOCESKAIA V.S., SCHWARTZ J.R., YU G., TORIUMI M., Lenz C.,

A Li J., Kremenetskaia I., Luros J., Lee J.M., Gonzalez A., Al

A Li J., Kremenetskaia I., Luros J., Lee J.M., Gonzalez A., Al

A Araujo R., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.

A Huizar L., Kim C., Palm C., Rowley D., Shinn P., Walker M.,

A Huizar L., Kim C., Palm C., Rowley D., Shinn P., Walker M.,

Bavis R.W., Ecker J.R., Federspiel N.A., Theologis A.;

"Arabidopsis thaliana chromosome 1 BAC T8K14 sequence.";

T "Arabidopsis thaliana chromosome 1 BAC T8K14 sequence.";

Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AC007202; AAD30219.1; -.

R HSSP; P08631; 1AD5

R InterPro; IPR000719; Euk_pkinase.

R InterPro; IPR000719; Euk_pkinase.

R InterPro; IPR000719; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.
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Best I
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Q9SAJ2;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00109; TYKKINASE.

ProDom; PD000001; Euk_pkinase; 1.

SMART; SM00221; STYCC; 1.

PROSITE; PS00107; PROTEIN KINASE_ATP; 1.

PROSITE; PS00101; PROTEIN KINASE_DOM; 1.

ATP-binding; Transferase; Tyrosine-protein kinase.

ATP-binding; 1248 AA; 137242 NW; 0EEE4A8899C50328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T8K14.1 protein.
T8K14.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00069; pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                      146
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 206
                                  136 LELAQKVGYEQI-----
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 ISIRKDISWQELRQKILEIY
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                                                                                                 DESLVR--GVTGDLHSFVSSSASVNGSVYGFPQYLCS--NFLLSSPNGTQ-----QASSL 135
                                                                                                                                   MNYNTGYMELRGLIGISHTGSECASDVSRFSTVENGTSDIERTNSSLHEFGNKLNHVQSA 145
                                                                                                                                                                           -GYNIEYTEF
                                                                                                                                                                                                       PFMPDQTGSASANMRPPNSNGSDVKAVHNFSIQTGEEFSLEFMRDRVIPQRSSNPNGAGD 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NLLTNTLVLDLLGLGLTLPANKNGIAHLAKSSNFYAQLSQQF
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                                                                                                                                                                                                                                                                            75; Conserv
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                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                          6.4%;
                                  -VYPDVASSSSTVFGLYQ-----
                                                                                                                                                                     -DCYSDASLQS-----LPDVFSTDSIFLPYLVSLGGVKSL 84
                                                                                                                                                                                                                                                                            69;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                          Score 116; DB Pred. No. 27; 69; Mismatches
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YQTRVVKYQLPGEDLDALVSVSSEED
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, Gonzalez A., Al
unn P., Hansen N.
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                              -QLLQSSSSAAVDIKASD- 182
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                                                                                                                                                                                                                                                                                                          Length 1248;
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Best Local S
Matches 47
                                                                                              Q9XYH6;
Q9XYH6;
01-NOV-1999
01-NOV-1999
01-JUN-2002
ATP-binding
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Q9RLV6;
01-MAY-2000
                         CPABC.
Cryptosporidium parvum.
Eukaryota; Alveolata; P
  Eukaryota; Alveolata; Apicomplexa; Cryptosporidiidae; Cryptosporidiim
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MEDLINE=20112344; PubMed=10647818;
Mungpraphapornchai P., Griffin H.G., Gasson
"Cloning, DNA sequence analysis, and deletic
diacetyl-acetoin reductase from Lactococcus
DNA Seq. 10:163-172(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 32.0 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein SEQUENCE 286 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR004872; Lipoprotein_9. Pfam; PF03180; Lipoprotein_9; 1.
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47; Conservative
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(TrEMBLrel. 12, La
(TrEMBLrel. 21, La
cassette protein.
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                                                                                                                                                                                                                          PRELIMINARY;
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                            Coccidia;
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deletion of a cocccus lactis.
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Best Local
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01-JAN-1998
01-MAR-2002
01-JUN-2002
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STRAIN=KSU-1;
MEDLINE=97376910;
                                                SEQUENCE FROM N.A
                                                                                                                     Eukaryota; Alveolata; Apicomplexa; Cryptosporidiidae; Cryptosporidiidae;
                                                                                                                                                                     Cryptosporidium parvum.
                                                                                                                                                                                                                      ATP-binding
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PROSITE; PS00211; ABC_TRANSPORTER; 2.

ATP-binding; Transport.

SEQUENCE 1431 AA; 162177 MW; 18AB
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InterPro; IPR003439; ABC transportr.
Pfam; PF00664; ABC membrane; 2.
Pfam; PF00005; ABC tran; 2.
ProDom; PD000006; ABC transportr; 2.
SMART; SM00382; AAA; 2.
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  PubMed=9233681;
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Pred. No. 42;
61; Mismatches
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SEQUENCE
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                   Sulfolobus solfataricus Archaea; Crenarchaeota;
                                                               Hypothetical SSO1375.
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PROSITE; PS00211; ABC_TRANSPORTER;
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Pfam; PF00005; ABC tran; 2.
ProDom; PD000006; ABC transport
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Sulfolobus
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Pred. No. 53;
61; Mismatches
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Q1-JUN-2002 (TrEMBLrel. 21, L
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Hypothetical protein MA4643.
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She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.
Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., I
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., I
Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstn
Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
"The complete genome of the crenarchaeon Sulfolobus solfata:
Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840 (2001).
EMBL, AE006751; AAKK1609.1;
                                                                                                                                                                                                                                                                                Q8TH79
                 STRAIN=C2A / ATCC
MEDLINE=21929760;
Galagan
                                                       SEQUENCE FROM N.A
                                                                                                            Archaea; Euryarchaeota; Methanococo
Methanosarcinaceae; Methanosarcina
                                                                                                                                              Methanosarcina acetivorans
                                                                                       NCBI_TaxID=2214;
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TCC 35092
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613 AA; 67767 MW; F478840A4CCB9BA3 CRC64;
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   Nusbaum
                 35395 / DSM 2834;
PubMed=11932238;
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Pred. No. 20;
72; Mismatches
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01-JUN-2002
01-JUN-2002
               STRAIN=MB4T / JCM11007;
MEDLINE=21992816; PubMed=11997336;
Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu
Chen Y., Xue Y., Xu Y., Lai X., Huang L.,
Tan H., Chen R., Wang J., Yu J., Yang H.;
Tan Complete sequence of T. tengcongensis c
Genome Res. 12:689-700(2002).
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                                                                                                                                                                                                                                                                                               Sugar-binding pour UGPB OR TTE0799
                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                     Thermoanaerobacteriales; NCBI_TaxID=119072;
                                                                                                                                                                                                                                                      Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Bacillus/Clostridium
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SEQUENCE 1
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EMBL; AE011187; AAM07977.1;
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AE013046;
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Pred. No. 65;
56; Mismatches
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X., №
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01-DEC-2001
01-JUN-2002
                                                                                                                                                                  STRAIN-CV. NIPPONBARE;
Sabaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
clone:P0684B02.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003023; BAB44026.1;
InterPro; IPR001644; CBS domain.
InterPro; IPR001607; C1-Channel_volt.
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                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poalea; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
                                                                                                                                     SEQUENCE
                                                                                                                                                              Ptam;
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FPQYLCSNFLLSSPNGTQQASSLLELAQKVGYEQIVYPDVASSSSFTVFGLYQQLLQSSS
                          DILLESRP---FTSGLSAAVLVQLIGVKVLATSLCRAFGLVGGYYAPSLFIGAATGMAYG
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                                                                                                                                PF00571; CBS; 2.
PF00654; voltage_CLC; 1.
NCE 718 AA; 76362 MW;
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                                                                                             Similarity
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                                                                             Score 110.5;
Pred. No. 29;
36; Mismatches
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Pred. No. 13;
8; Mismatches 143;
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Best Local :
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Submitted (MAR-1998) to the EMBL/GenBank/DDBJ
EMBL; AF053986; AAC08413.1; -.
InterPro; IPR001878; ANF receptor.
InterPro; IPR000337; GPCR_Mgr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
Putative pheromone receptor V2R2.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrat
Mammalia; Eutheria; Rodentia; Sciurognathi; Murid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           070410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00003; 7tm_3; 1.
Pfam; PF01094; ANF_receptor; 1.
PRINTS; PR00248; GPCRMGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97436753; PubMed=9292726;
Ryba N.J., Tirindelli R.;
"A new multigene family of putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      070410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=VOMERONASAL NEURONS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090
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                                                                                                    264
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EYFPYFGGTIGFATPRSVIPGLKEFLYDVHPNKDPNDVLTIEFWQTAFNCTWPNSSVPYN
                                                  NYY-----VGYSESMCEI---KDIIRDQQ
                                                                                                                                                    PQSGDQVNKDITQK------YRTILDSTVVASQREYINSVKQGKPIS
                                                                                                                                                                                                    SEAIVNLIKHFGW--VWVGAIAADDDYGKYGVKTFKEKMESANLCVAFSETIPKVYSNEK 263
                                                                                                                                                                                                                                                       ASSLLELAQKVGYEQIVYPDVASSSSFTVFGL--YQQLLQSS-----
                                                                                                                                                                                                                                                                                                            AALVGSGGSSLSVAASRILGLYYMPQVGYTSSCSILSDKFQFPSY----LRVLPSDNLQ
                                                                                                                                                                                                                                                                                                                                                            PYLVSLGGVK-SLDESLVRGVTGDLHSFVSSSASVNGSVYGFPQYLCSNFLLSSPNGTQQ 131
                                                                                                                                                                                                                                                                                                                                                                                                              IKEINERKDILPNHTLGYQI----FDSCYTISKAMESSLVFLTGQEEFKPNFRNSTGSTL 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QENLTVAEAMKTKY I SVSKTTPVVEALNLML
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                                                                                                    MQKAVKAVKTSTAKVIVLYTSDIDLSLFVLEMIHHNITDRTWIATE-AWITSALIAKP--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62;
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Pred. No. 41;
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Best Local
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EMBL; U67717; AAC49813.1; -.
HSSP; P13797; 1AOA.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fimbrin/plastin-like (Fragment). Triticum aestivum (Wheat).
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01-JAN-1998 (TrEMBLrel. 05, Last
01-JUN-2002 (TrEMBLrel. 21, Last
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "CDNA clones encoding 1,3-beta-glucanase and a fimbrin-like Cytoskeletal protein are induced by Al toxicity in wheat roots.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cruz-Ortega R., Cushman J.C., Ownby J.D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001589; Actbind_actnin.
InterPro; IPR001715; Calponin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CV. VICTORY; TISSUE=ROOT;
MEDLINE=97422889; PubMed=9276954;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FF00307; CH; 4.
F; SM00033; CH; 3
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                                                                       LRCVDFANKEVK 346
                                                                                                                                                                    EV---IKNLLTNTLVL--DLLGLGLTLPANKNGIAHLAKSSNFYAQLSQQFDAKESEVRV
                                                                                                                                                                                                                                                                   GKPISNYYVGYSESMCEIKDIIRDQQYNVQLIGTSDKPYVYTDVLALNSNLCDEKQKVAV
                                                                                                                                                                                                                                                                                                                   FVAQIFQHRNGLTSDIKQVTLTQSASRDDVLVSREERAFRMWINSLGVES---YLNNVFE
                                                                                                                                                                                                                                                                                                                                                                                                                     AYAYLLKALAPE-TSPETTLETKNPDERAKMVLEQAEKLDCKRYLTPKDITEGSANLNLA
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                                                                                                                ELKFSLVNLAGNDIVQGNKKLIVALLWQLMRFNILQLLNRLRSHSKGSQGKQITDADI--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 109; DB
Pred. No. 19;
72; Mismatches
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RESULT 12

O44800
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AC 04480
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=BRISTOL N2;
Du Z., Le T.T.;
"The sequence of C. e
Submitted (JAN-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson .
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., McMurray A., Mortinore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F14D2.6.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (DEC-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 368:32-38(1994).
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MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
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259
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VYTD--VLALNSN----
                                                   NEEYILNLKNTKVICGFGFFGAFGASCYFGERYGDIPLIRFSSNKLLRNVTLPQMKNPPF
                                                                                                          QREYINSVKQGKPISNY-YVGYSESMCEIKD-----
                                                                                                                                                                                                                      LQSSSSAAVDIKASDLPQSGDQVNKDITQK----
                                                                                                                                                                                                                                                                          SFNFTSIHDNPN------LRRLGLDSL--KQLGPAGKFTIHIANNHPDFCLSTSE
                                                                                                                                                                                                                                                                                                                                CSNF--LLSSPNGTQQASSLLELAQKVGYEQIVYPDVASSSSFTV-----
                                                                                                                                                                                                                                                                                                                                                                                          STTTQFPTIQTALQYLSSLSLLKKLNGMLEIYETGLENVSFLGNLETHNGKNGGLPEKYW
                                                                                                                                                                                                                                                                                                                                                                                                                                           SLPDVFSTDSIFLPYLVSLGGVKSLDESLVRGVTG-DLHSFVSSSASVNGSVYGFPQ-YL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLTSIYNSIDWWSQETSKWDIINNTKLDVGIVCRVAERDI-YADFNAYGNRKVVAADSYK 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tted (DEC-1997) to the EMBL/Ge
AR040643; AAB94960.1; -
PERO; IPR000494; EGFR L domain.
PF01030; Recep L domain; 3.
ENCE 998 AA; Il3094 MW; BE4
                                                                                                                                                                   LQVFARTNLKIYGFEV---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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--LCDEKQKVAVEVIK 283
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Last sequence update)
Last annotation updat
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EMBL/GenBank/DDBJ
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RESULT 14
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Best Local
                                                                                                                                      ul-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Conserved hypothetical membrane protein.
TAll36.
                                                                                                                                                                                                                                                                   Q9HJ37
Q9HJ37;
                                                                  TAIIJo.
Thermoplasma acidophilum.
- `---- Furvarchaeota; Thermoplasmata; Thermoplasmatales;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of the nematode C.ele investigating biology."; Science 282:2012-2018(1998).

EMBL; 277663; CAB01214.1; -.

InterPro; IPR000960; Flav_cont_mnoxgn.
Pfam; PF00743; FW0-like; I.
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MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q20730
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                                                                                                                                                                                                                                                                                                                                                                                                                  IIGCLPPMKHYLFFYPRFWMKLFMGANVPYAY
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NCE 528 AA;
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l Similarity 21.7%;
59; Conservative 4
FROM N.A
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AA; 60119
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, Last sequence up
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Pred. No. 28;
47; Mismatches
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MEDLINE-20479972; PubMed=11029001;
Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volk
Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister
"The genome sequence of the thermoacidophilic scavenger Therm
                                                                                                                                                                                                                                                                       MEDLINE=21116945; PubMed=11179301;
Bensing B.A., Rubens C.E., Sullam P.M.;
"Genetic loci of Streptococcus mitis that
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Nature 407:508-513(2000).
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RGITGKIQSILNPEASAAGQSAG--QSLGSSLVGVMTKVIAAAGIGKAFSAAISEGAALQ
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77; Conserv
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Similarity 21.3%;
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X007505; AAG18638.1; -.

E 1007 AA; 107445 MW; E
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3; Mismatches
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Pred. No. 2.3e+02;
9; Mismatches 148;
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Search completed: January 24, 2003, 19:42:43 Job time : 41 secs

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Reith M.E., Munholland J.;
"Complete nucleotide seque
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                         use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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FUNCTION: THIS PROTEIN IS POSTULATED TO ACT
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THE PHYCOBILISOME ARCHITECTURE.
                                                                                     SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the St
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      Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Barooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares R., Stevens K., Sharp S., Stevens K., Simmonds M., Squares R., Squares R., Stevens K., Sharp S.
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Putative translational activator C18G6.05C (G
SPAC18G6.05C.
                                                                                                                                                         STRAIN=972;
MEDLINE=21848401; PubMed=11859360;
Wood V., Gwilliam R., Rajandream M
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InterPro; IPR001659; Phycobilisome.
Pfam; PF00427; PBS_linker_poly; 3.
Pfam; PF00502; Phycobilisome; 1.
ProDom; PD000340; Phycobilisome; 2.
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Phycobilisome; Electron transport; Photosynthesis;
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Pred. No. 1.6
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"The genome sequence of Schizosaccharomyces pombe.";
Nature 415:871-880 (2002).
"C. -!- SIMILARITY: STRONG, TO YEAST GCN1."
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SEQUENCE
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Weltjens I., Vanstreels E., Rieger K.
Gabel C., Fuchs M., Fritzc C., Holze
Borzym K., Langer I., Beck A., Lehra
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PROSITE; PS50077; HEAT_REPEAT;
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183 LPQSGDQVNKDITQKYRTILDS--TVVASQREYINSVKQGKPISNYYVGYSESMCE--IK 238
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                                                                                         ANKSLLRFGDVISNPEIQTLVPTLLKALSDCTRYTDDALEALLKTSFVHYLDPPSLALVI 1601
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Pred. No. 15;
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01-FEB-1996 (R
Phycobilisome
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P28561;
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the European Bioinformatics Institute. There a
use by non-profit institutions as long as a
modified and this statement is not removed. Us
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InterPro; IPR001297; PBS_linker_poly.
InterPro; IPR001659; Phycobilisome.
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 157 SFTVFG---
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SIMILARITY: OF THE REPEATED DOMAINS TO N-TERMINAL REGIONS
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                                                      ASVNGSVYGFPQYLCSNF----
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(Rel. 24, Last sequence update)
(Rel. 33, Last annotation update)
me linker polypeptide (Anchor poly
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Pred. No. 5.5;
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DEBOC
                                                                                                              MEDLINE=92307400; PubMed=1612414;
Park J.C., Bai S., Tai C.Y., Chun S.B.;
"Nucleotide sequence of the extracellular alpha-amylase gene in "Nucleotide sequence of the extracellular alpha-amylase gene in "Nucleotide sequence of the extracellular ATCC 26077.";
FEMS Microbiol. Lett. 72:17-23 (1992).
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1.4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
-!- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
-!- ENZYME REGULATION: ALPHA-AMYLASE EXPRESSION UNDERLIES CATAL REPRESSION BY GLUCOSE.
                                                                                                                                                                                                                                                                                                                     MEDLINE=92120467; Po
Wu F.M., Wang T.T.,
"The nucleotide seque.";
                                                                                                                                                                                                                                                                                                                                                                                                                             Strasser A.W.M., Selk R., Dohmen R.J., Niermann T., Bielefeld M., Seeboth P., Tu G., Hollenberg C.P.; "Analysis of the alpha-amylase gene of Schwanniomyces occidentalis and the secretion of its gene product in transformants of different yeast genera.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=ATCC 26076;
MEDLINE=90032659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Alpha-amylase 1 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
           This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
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AS THE ALPHA-AMYLASE FAMILY.
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          Swiss Institute or Lawrence Institute. The Bioinformatics Institutions as long
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ungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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; X16040; CAA34162.1;
; X62079; CAA43995.1;
; S38381; AAB22383.2;
                                                     ICNO
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Spiers A.J., Kahn S.G., Bohammon J., Travisano M., Raine
"Adaptive divergence in experimental populations of Pseu
fluorescens. I. Genetic and phenotypic bases of wrinkly
           (Ilers).
ILES OR BB0833
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 Borrelia burgdorferi
                                           Isoleucyl-tRNA synthetase
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                                                                                                                                                                                                                                                                                                                                                             326 RYTPQQVSTNSSLLIGLNDQF-MKSVALPSVSNLGGGQTLLDQLKKDESLPREVT-TLLP 383
                                                                                                                                                                                       501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Binds the cellulose synthase activator, bis-(3'-5') cyclic diguanylic acid (c-di-GMP) (By similarity). SUBUNIT: Tightly associated with the cellulose synthase catal subunit (By similarity).
PATHWAY: Bacterial cellulose biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE ACSB/BCSB FAMILY.
                                                                                                                                                                                      QSVADKDLLVLATAANQPLLKQWQQYLPATSDGEQHQFLLS
                                                                                                                                                                                                                  POSGDQ------VNKDITQKYRTILDSTVVASQREYINS
                                                                                                                                                                                                                                             VFNDSGFPFTRLADLSESAVVMPDNYGTDELTAYLTVLGRFGEATGYPATAVKVVQAKDV
                                                                                                                                                                                                                                                                                                    ISSASPKSKLOVRFMYDYIKEGECRDIIVDNMRGSVDPDSTLDV---TGYQHYIAMPNLG
                                                                                                                                                                                                                                                                                                                               FVSSSASVNGSVYGFPQYL----CSNFLLSSPNGTQQASSLLELAQKVGYEQ------
                                                                                                                                                                                                                                                                                                                                                                                         EYTEFDCYSDASLQ-SLPDVFSTDSIFLPYLVSLGGVKSL-----DESLVRGVTGDLHS
                                                                                                                                                                                                                                                                                                                                                                                                                     PYDAPNWLPSNRPVRLGELIEQ-QKLSVSGYNPGAISVDMRLPPDLFNWREEGVPLKLKY 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PY-LPSWNENGNEVKLINLIKDVLPTQVSGYN------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s requires a license agreement (S
an email to license@isb-sib.ch).
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(Rel. 41, 1
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40, Last
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protein
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                                         sequence update)
annotation update)
(EC 6.1.1.5) (Isoleucine--tRNA)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence update)
annotation update)
ein (Cellulose synthase regulatory subunit)
disease spirochete)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 104; DB Pred. No. 7.4; 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FBE0BBCEE76EF3D8
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f Pseudomonas
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Best Local (
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SEQUENCE
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Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwin
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson
van Vugt R., Palmer N., Adams M.D., Goayne J.D., Weidman J.,
Utterback T., Watthey L., McDonald L., Attiach P., Bowman C.,
Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.
                                                                                                                                                                                                                                                                                                                                                                                   SITE
                                                                                                                                                                                                                                                                                                                                                                                                             TIGREAMS; TIGRO0392; iles; 1.

PROSITE; PS00178; AA TRNA LIGASE I; FALSE NEG.
Aminoacyl-tRNA synthetase; Protein biosynthesis;
Metal-binding; Zinc; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002300; tRNA-synt_la.
InterPro; IPR001412; tRNA-synt_l.
InterPro; IPR002301; tRNA-synt_ile.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith H.O., Venter J.C. "Genomic sequence of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00133; tRNA-synt_1; 1. PRINTS; PR00984; TRNASYNTHILE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 390:580-586(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     burgdorferi.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Spirochaetales;
833
                             229
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                                                                                                                                              139
                                                                                                                                                                           675
                                                                                                                                                                                                                                    634 YSDNG
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                                                                                                                                                                                                                                                       19 WNENGNEVKLINLIKDVLPTQVSGYNIEYTEFDCYSDASLQSLPDVFSTDSIFLPYLVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: ATP + L-isole diphosphate + L-isoleucyl-tRNA(I) COFACTOR: BINDS 1 ZINC ION (BY S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: MONOMER (BY SIMILARITY)
SUBCELLULAR LOCATION: Cytoplasmi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; AE001181; AAC(; P56690; 1ILE.; BB0833; -.
                                                                                                                                                                           AKNNNLDKWII----SELESLKK------ILNTEIDKYNLTKSIESLLEF
                                                                                                                                                                                                     GGVKSLDESLVRGVTGDLHSFVSSSASVNGSVYGFPQYLCSNFLLSSPNGTQQASSLLEL 138
VTKNQNEQNMLMEMQE I I LDE I NAKEMKI KANEEEL I TYKAKAN FKELGKKLGKDMKAVS
                                                                                  SSSSAAVDIKASDLPQSGDQ-VNKDITQKYRTILDSTVVASQREYINSVKQGKPISNYYV
                                                                                                                 IDKLNNWYIRRSRRFWKSENDKDKNDAYETLYYAIKTLMILLAPFIPFITEEIYQNLKT
                           ----GYSESMCEIKDIIRDQ-
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594
597
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597
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18.8%;
                                                                                                                                                                                                                                                                                                                                                         122331 MW;
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                                                                                                                                                                                                                                                                                             59;
                                                                                                                                                                                                                                    ---NIII PIWNAYSFFTTYAIIDKFKP-----PKNLSL
                                                                                                                                                                                                                                                                                           Score 101; DB
Pred. No. 22;
59; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease spirochaete,
                                                                                                                                                                                                                                                                                                                                                      "KMSKS" REGION.
ATP (BY SIMILARITY).
WW; 6C0F7D820CA32F75
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-tRNA(Ile).
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                                                                                                                                                                                                                                                                                              120;
                          --QYNVQLIGT---SDKPYVY
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                                                                                                                                                                                                                                                                                                                         Length 1042;
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                                                                                                                     RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., RA Brooks K., Brown D., Brown S., Chillingworth T., Fraser A., RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., RA Holroyd S., Hornsby T., Howarth S., Hickle E.J., Hout S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J., RA Oliver K., O'Nell S., Pearson D., Quail M.A., Rabbinowitsch E., RA Gliver K., O'Nell S., Pearson D., Quail M.A., Rabbinowitsch E., RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moest D., Hilbert H., RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Palakovski G.V., Ussery D., Barrell B.G., Nurse P.; "The genome sequence of Schizosaccharomyces pombe.";

RI Nature 415,871.880 (2002)
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                                                             Query Match
Best Local
                                            Matches
                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YAB5_SC
Q09807;
                                                                                                                                                                                          EMBL; Z54354; CAA91170.1; -.
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                                                                                                                   Hypothetical
SEQUENCE 7
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01-NOV-1995 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                       nterPro; IPR004328; BRO1.
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                                                                                                                   81769 MW;
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                                                       5.5%;
19.0%;
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, Last annotation update)
C2G11.05c in chromosome
                                        68;
                                  Score 99.5; DE
Pred. No. 16;
58; Mismatches
                                                                                                                                                                                                                                           agreement (See http://www.isb-sib.
                                                                                                                 E13EB4C4AE085671 CRC64;
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Q45706;
30-MAY-2000
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30-MAY-2000
Pesticidial
                                                                                                                                                      scarabaeid beetles.",

J. Appl. Bacteriol. 76:307-313(1994).

-:- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MII-
-:- EPITHELIAL CELLS OF INSECTS. ACTIVE ON VARIOUS SCARABAEID BEI
SUCH AS ANOMALA CUPREA, A. RUFOCUPREA AND POPILLIA JAPONICA.

-:- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
                        use
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                                                                                                                                                                                                                                                             Minami M.,
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Hori H., Suzuki N., Ogiwara K.,
                                                                                                                                                                                                                                                                                                                                                                                           Sato R.,
                                                  between
                                                             This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                  thuringiensis serovar japonensis
                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-14 AND 56-64, AND CHARACTERIZATION MEDLINE=94259659; PubMed=8200856;
                                                                                                                                                                                                                                                                                                                                         Hori H., Asano S., Ohba M., Iwahana H.; "Cloning, heterologous expression, and localization of a novel crystal protein gene from Bacillus thuringiensis serovar japonensis strain buibui toxic to scarabaeid insects.";
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94100786;
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Bacteria; Firmicutes; E
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                                                                                                                                                                                                                                                 Minami M., Asano S., Sato R., Ohba M., Iwahana "Characterization of larvicidal toxin protein i
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Takeuchi K., Ogiwara K
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(Rel. 39, Last annotation update)
crystal protein cry8Ca (Insecticidal delta-endotoxin
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P28742;
01-DEC-1992
01-DEC-1992
MEDLINE=94205266; PubMed=8154187; Scherens B., el Bakkoury M., Vierendeels F., Dub "Sequencing and functional analysis of a 32,560 left arm of yeast chromosome II. Identification frames, including the KIP1 and SEC17 genes."; Yeast 9:1355-1371(1993).
                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
Saccharomycetales; Saccharomycetaceae; Saccharon
                                                                                                                                                                                                                                                                         01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Kinesin-like procein KIP1.
KIP1 OR CIN9 OR YBL065W OR YBL0504 OR YBL0521.
                                                                                      SEQUENCE FROM N.A.
STRAIN=S288C;
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Pfam; PF00555; endotoxin;
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P07130; 1DLC.
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P.B., Rose M.D.;
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EMBL; Z32824; CAA84883.1; -.
PIR; A42640; A42640.
HSSP; P17119; 3KAR.
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STRAIN-5286; PubMed=1643659;
MEDLINE=92354062; PubMed=1643659;
Saunders W.S., Hoyt M.A.;
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PRINTS; PR00380; KINESINHEAVY.
SMART; SM00073; HPT; 1.
SMART; SM00129; KISC; 1.
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Cell 70:451-458(1992)
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InterPro; IPR002570; Hpt.
InterPro; IPR001752; kinesin_motor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: REQUIRED FOR ASSEMBLY OF THE MITOTIC SPINDLE. INTERA MITH SPINDLE MICROTUBULES TO PRODUCE AN OUTWARDLY DIRECTED FORCE ACTING UPON THE POLES. FOLLOWING SPINDLE ASSEMBLY, CINB KIP1 APPARENTLY ACT TO OPPOSE A FORCE THAT DRAWS SEPARATED POLEACK TOGETHER. THIS FORCE SEEMS TO BE MEDIATE BY KAR3. SUBUNIT: MIGHT BE DIMERIC.
SUBCELLULAR LOCATION: SPINDLE MICROTUBULES THAT LIE BETWEEN TH POLES.
SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. BIMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBFAMILY
                                                                                                                                                                                                                                NEVKLINLI---KDVLPTQVSGYNIEYTEFDCYSD-----ASLQSLPDV----
                                                                                                   STLKSLLNITTNLLMNQMN
                                                                                                                                                                                                        NOLDINNLLOSEKEKLIAIIONFNVDFSNF--YSEIOKIHHTNLELMNEVIOORDFSLEN
NVLIENQQSGSSKLIKEQDLEIKKLKNDLINERRISNQFNQQL--AEMKRYFQDHVSRTR
                        ---ISNYYVGYS---
                                                QSDSTSHYRKDLNEIYQSHQQFLKNLQNDIKSCLDS-IGSSILTSINEISQNCTTNLNSM
                                                                        QSSSSAAVDIKASDLPQSGDQVNKDITQKYRTILDSTVVASQREYINSVKQGKP-
                                                                                                                           SVYGFPQYLCSNFLLSSPNGTQQASSLLELAQKVGYEQIVYPDVASSSSFTVFGLYQQLL
                                                                                                                                                    SQKQYNTNQNMQLKISQQVLQTLNTLQGŚĹNNYNŚKCSEVIKĠVTEEĹTRNVNTHKAKHD
                                                                                                                                                                              IFLPYLV-----SLGGVKSLDESLVRGVTGDLHSFVSSSASVNG
                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                      1 cycle.
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808
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                                                                                                                                                                                                                                                                                                                                     423
510
670
780
828
                     -ESMCEIK----DIIRDQ----QYNVQLIGTSDKPYVYTDVLALN
                                                                                                                                                                                                                                                                      21.8%;
                                                                                                                                                                                                                                                                                                              125794
                                                                                                                                                                                                                                                                                  5.49
                                                                                                    -----ELVRSI-----
                                                                                                                                                                                                                                                          50;
                                                                                                                                                                                                                                                                                                                         KINESIN-MOTOR (BY SIMILARITY).
COLLED COIL (POTENTIAL).
COLLED COIL (POTENTIAL).
COLLED COIL (POTENTIAL).
COLLED COIL (POTENTIAL).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                            ATP
MW;
                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                            212F8279766137FC CRC64;
                                                                                                                                                                                                                                                                                  97.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for structural integrity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as its content
                                                                                                                                                                                                                                                        112;
                                                                                                                                                                                                                                                                                                                                                                                                                ATP-binding; Coiled
                                                                                                                                                                                                                                                                                  1;
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                                                                                                                                                                                                                                                                                 Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            outstation
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                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   coil;
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                        267
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268

SNLCDEKOKVAVEVIKNLLTNTLVLD

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RESULT 11
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Inositol 1,4,5-trisphosphate receptor type 2 (Ty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IP3S_HUMAN
Q14571; O947
01-NOV-1997
                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI TaxID=9606;
                  InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Futatsugi A., Kuwajima G., Mikoshiba K.;
"Muscle-specific mRNA isoform encodes a protein composed mainly
N-terminal 175 residues of type 2 Ins(1,4,5)P3 receptor.";
Biochem. J. 334:559-563(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94363219; PubMed=8081734; Yamamoto-Hino M., Sugiyama T., Hikiti Hasegawa K., Sekine S., Sakurada K., Masegawa M., Mikoshiba K.;
                                                                MIM;
                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                              Genew;
                                                                                            EMBL; AB012610; BAA33961.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98399819; PubMed=9729462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recept.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (SHORT ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning and characterization of 1,4,5-trisphosphate receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
      InterPro;
                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           756
                                                                                                                                                                                                                                                         DOMAIN: THE RECEPTOR CONTAINS A CALCIUM CHANNEL IN ITS C-
EXTREMITY. ITS LARGE N-TERMINAL CYTOPLASMIC REGION HAS TH
BINDING SITE IN THE N-TERMINUS AND MODULATORY SITES IN TH
PORTION IMMEDIATELY UPSTREAM OF THE CHANNEL REGION.
PTM: PHOSPHORYLATED ON TYROSINE RESIDUES (BY SIMILARITY).
MISCELLANBOUS: CALCIUM APPEARS TO INHIBIT LIGAND BINDING
RECEPTOR, MOST PROBABLY BY INTERACTING WITH A DISTINCT
CALCIUM-BINDING PROTEIN WHICH THEN INHIBITS THE RECEPTOR.
SIMILARITY: BELONGS TO THE INSP3 RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                              ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM SHORT FORM/TIPR; ARE PRODUCED BY ALTERNATIVE STISSUE SPECIFICITY: THE SHORT ISOFORM IS FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: RECEPTOR FOR INOSITOL 1,4,5-TRISPHOSPHATE, MESSENGER THAT MEDIATES THE RELEASE OF INTRACELLULAR SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                     AND HEART
DOMAIN: T
                                                                                                                                                                                                                                                                                                                                                                                                                                                              reticulum.
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                                                              600144;
                                                                                                            D26350; BAA05384.1;
                                                                            HGNC: 6181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Channels 2:9-22(1994).
                 IPR000699; Ca-rel_channel.
IPR001682; Ca/Na_pore.
IPR000493; InsP3_receptor.
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Catarrhini; Hominidae;
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                                                                                                                                                      http://www.isb-sib.ch/announce,
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N THE MIDDLE
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MBL outstation -
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RESULT 12
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Best Local :
                                                              15-JUL-1998
15-JUL-1998
15-JUL-1998
                                                                                                DIMH_CAI
017397;
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VARSPLIC
VARSPLIC
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DOMAIN
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SMART; SM00472; MIR; 4.
          Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Receptor;
                               Caenorhabditis elegans
                                            F52H2.6
                                                     Diminuto-like
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                                                                                                            CAEEL
                                                                                                                                                                   RYFKGDYSIGV-----NG--HLSGAYSKTAQVGGSFSGQDSD 1736
                                                                                                                                                                                       -----GLGLTLPANKNGIAHLAKSSNFYAQLSQQFDAKESE 331
                                                                                                                                                                                                              KLINHTKK-
                                                                                                                                                                                                                                   QLIGTSDKPYVYTDVLALNSNLCDEKQKVAVEVIKNLLT------
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                                                                                                                                                                                                                                                                                                     NRG---IAIPVDLDSQVNTLF-----MKSHSNMVQRAAMGWRLS--ARSGPRFKEALGG
                                                                                                                                                                                                                                                                                                                          KVGYEQIVYPDVASSSSFTVFGLYQQLLQSSSS----AAVDIKASDLPQSGDQVNKDI--
                                                                                                                                                                                                                                                                                                                                                IVSGFFNSPFSDNSTSLQTHQPVFIQLLQSAFRIYNCTWPNPAQKASVESCIRTLAEVAK 1545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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Transmembrane; Glycoprotein; Phosphorylation;

Calcium
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(Rel. 36, Last sequence update)
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           Nematoda; Chromadorea; Rhabditida; Rhabditoidea; rinae; Caenorhabditis.
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CYTOPLASMIC (P
POTENTIAL.
EXTRACELLULAR
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IVVGDK -> DASFWI (IN SHORT
MISSING (IN SHORT ISOFORM)
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EXTRACELLULAR
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                                                                update)
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RESULT 13
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Best Local S
Matches 61
                                                                                                                                                                                                                01-NOV-1995
01-NOV-1995
16-OCT-2001
SEQUENCE FROM N.A.

STRAIN-K12 / MG1655;

MEDLINE=97426617; PubMed=9278503;

Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D. Mau B., Shao Y.;

"The complete genome sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A.
STRAIN=Bristol N2;
                                                                                                                                                                                     Hypothetical c
YHCD OR B3216.
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Submitted (SEP-1997) to
-!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                           P45420;
                                                                                                                                             Escherichia
                                                                                                                                                        Bacteria; Proteobacteria;
                                                                                                                                                                      Escherichia coli
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SEQUENCE 5
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InterPro; IPR001575; Oxid_
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                                                                                                                            _TaxID=562;
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                                                                                                                                                                                                                                                                                                                                                                                                    DGPDTHDEVVNPIGRWYKKWFYTHVEDLINKKHESIEYI----PLRDYYHRHSKSIFWEL
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525 AA;
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(Rel. 32, Last sequence update)
(Rel. 40, Last annotation updat
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                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                  membrane
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_binding_4; 1.
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                                                                                                                                                        gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50;
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Pred. No. 16;
50; Mismatches
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                                                                                                                                                                                                 cion update)
protein yho
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                                                        Burland V.,
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RESULT 14

COPP YEAST

ID COPP YEAST STANDARD; PRT; 889 AA.

AC P41811;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 36, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Coatomer beta' subunit (Beta'-coat protein) (E GN SEC17 OR YGL137W OR G2827.

OS SECCHAROMYCES cerevisiae (Baker's yeast).

OC Bukaryota; Pungi; Ascomycota; Saccharomycotina OC Saccharomycetales; Sacchar
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SEQUENCE
                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U18997; AAA58018.1; -.
EMBL; AE000401; AAC76248.1; -.
EcoGene; EG12810; yhcD.
InterPro; IPR000015; Fimb_usher.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restude by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>:</u>
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-!- FUNCTION: INVOLVED IN T
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Pred. No. 30;
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or send a
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CLATHRIN-COATED VESICLES, WHICH FURTHER MEDIATE BIOSYNTHETIC
PROTEIN TRANSPORT FROM THE ER, VIA THE GOLGI UP TO THE TRANS GOLGI
NETWORK. COATOMER COMPLEX IS REQUIRED FOR BUDDING FROM GOLGI
NETWORK. COATOMER COMPLEX IS REQUIRED FOR BUDDING FROM GOLGI
NETWORK. COATOMER COMPLEX IS REQUIRED FOR BUDDING FROM GOLGI
NETWORKS, AND IS ESSENTIAL FOR THE RETROGRADE GOLGI-TO-ER
TRANSPORT OF DILYSINE-TAGGED PROTEINS.

TRANSPORT OF DILYSINE-TAGGED PROTEINS.
SUBUNIT: OLIGOMERIC COMPLEX THAT CONSISTS OF AT LEAST THE ALPHA,
BETA, BETA', GAMMA, DELTA, EPSILON AND ZETA SUBUNITS.
ON THE CYTOPLASMIC SIDE OF THE GOLGI, AS WELL AS ON THE
VESICLES/BUDS ORIGINATING FROM IT (BY SIMILARITY).

SIMILARITY: CONTAINS 6 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                         PRINTS; PR00320; GPROTEINBRPT.
ProDom; PD000011; WD40; 3.
SMART; SM00320; WD40; 6.
SMOSITE; PS00678; WD_REPEATS_1; 1.
PROSITE; PS50088; WD_REPEATS_7; 5.
PROSITE; PS50088; WD_REPEATS_REGION;
PROSITE; PS50294; WD_REPEATS_REGION;
Transport; Protein transport; Golgi s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=S288c / FY1679;
MEDLINE=96437978; PubMed=8840506;
BESCRIbano V., Eraso P., Portillo F., Mazon M.J.;
"Sequence analysis of a 14.6 kb DNA fragment of Saccharomyces "Sequence analysis of a 14.6 kb DNA fragment of putative cerevisiae chromosome VII reveals SEC27, SSM1b, a putative
                                                                                                                                       REPEAT
REPEAT
                                                                                                                                                                         REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collat between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95014199; PubMed=7929113;
Duden R., Hosobuchi M., Hamamoto S., Winey M., Byers B., Schekman
"Yeast beta- and beta'-coat proteins (COP). Two coatomer subunits
                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U11237; AAA61711.1; -.
EMBL; W92670; CAA63359.1; -.
EMBL; Z72659; CAA96848.1; -.
SGD; S0003105; SEC27.
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                                                                                                         SEQUENCE
                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00400; WD40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94009692; PubMed=8405452;
Harter C., Draken E., Lottspeich F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-27.
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                                                                                                                                                                                                                                                                                                                                                                               nterPro; IPR001680; WD40
 19 WNENGNEVKLINLIKDVLPTQVSGYNIEYTEFDCYSDASLQ-SLPDVFSTDSIFLPYLVS 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        European Bioinformatics Institute. The European Bioinformatics Institutes as long to mon-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s requires a license agreement (S an email to license@isb-sib.ch).
                                                     Similarity
                                                                                                  ; Endoplasmic reticulum.

11 41 WD 1.

53 83 WD 2.

53 125 WD 3.

158 169 WD 4.

182 214 WD 5.

226 256 WD 6.

889 AA; 99444 MW; 6A5E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for endoplasmic reticulum-to-Golgi protein traffic.";
Chem. 269:24486-24495(1994).
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                                     Conservative
                                                   5.4%;
19.8%;
                                   58;
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Pred.
                                                                                                       6ASES0BBEB02CB58 CRC64;
                                 ed. No. 36;
Mismatches
                                                   No.
                                                                                                                                                                                                                                             stack; Membrane; Repeat;
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                                                                   DB 1;
                                   127;
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                                   79;
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                                Gaps
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P75056;
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
MEDLINE-97105885 Hilbert H., Plagens
                                                     LIPID
SEQUENCE
                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content
                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                        pneumoniae.";
Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997
16-OCT-2001
                                                                               CHAIN
                                                                                             SIGNAL
                                                                                                                                             Pfam; PF02030; Lipoprotein_8; PRINTS; PR00905; MYCMG045.
                                                                                                                                                         InterPro; IPR000044; Lipoprt_MG045.
Pfam; PF02030; Lipoprotein_8; 1.
                                                                                                                                                                                   EMBL; AE000011; AAB95744.1; -
                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
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                                                                                                                  Hypothetical protein; Lipoprotein; Membrane;
                                                                                                                                 PROSITE; PS00013; PROKAR_LIPOPROTEIN;
                                                                                                                                                                                                                      entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                               "Complete sequence analysis of the
                                                                                                                                                                                                                                                                                                                                                                               Herrmann R.;
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                                                                                                                                                                                                                                                                                                                (Potential).
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   61;
                 Similarity
                                                                                                      proteome.
                                                      485
   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lipoprotein MG045 homolog precursor (D09_orf485).
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                                                                                                                                                                                                                                                                                                                              LOCATION: Attached to the membrane by a lipid anchor
                                                                  485
23
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                                                      55019
               5.3%;
21.8%;
                                                      ME.
   47;
  Score 96; DB
Pred. No. 16;
17; Mismatches
                                                     HYPOTHETICAL LIPOPROTEIN MG045
N-ACYL DIGLYCERIDE (POTENTIAL)
; 1AD4E0AB211B64F8 CRC64;
                                                                                             POTENTIAL.
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     116;
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                             Length 485
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24 NEVKLINLIKDVLPTQVSGYNIEY--TEFDCYSDASLQ--SLPDVF--STDSIFLPYLVS

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Db 201 HEVK--NTTVDVNPT---GSTLNYFGNVYESFANLGLKRDNLNTLFVNSDSNIIINELAN 255

Qy 78 ---LGGVKSLDESLVRGVTGDLHSFVSSSASVNGSVYGFPQYLCSNFLLSSPNGTQQASS 134

Db 256 GRRQGGIVYNGDAVYAALGGDLRDEINNNLPNG--------DNFHIVQPKHSPVALD 305

QY 135 LLELAQKVGYEQIVYPDVASSSFTVFGLYQQLLQSSSSAAVDIKASDLPQGSDQVNKDI 194

Db 306 FLIINQ----QQTHFRDAA--------HQLIYQLALEGADQTAEELLKTDEEKGTSD 350

QY 195 TQKYRTILDSTVVASQR-EYINSVKQGKPISNYYVGY--SESMCEIKDIIRDQQYNVQL 250

QY 196 TQKYRTILDSTVVASQR-EYINSVKQGKPISNYYVGY--SESMCEIKDIIRDQQYNVQL 250

QY 197 TQKYRTILDSTVVASQR-EYINSVKQGKPISNYYVGY--SESMCEIKDIIRDQQYNVQL 250

QY 251 IGTSDKP------TYGAMQNFSYVNYVSPLKNISDETTGIVFKENKQADTKQVVKQQSQSEQQ 404

QY 251 IGTSDKP------YVYTDVLALNSNLCDEKQKVAVEVIK 283

Db 405 SESAEKEETEQDDFYTATLKSLLKADSLDDKAKKLVDTIK 444
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Maximum Match 100%
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Perfect score:
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106
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seq length: 2000000000
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                                     hypothetical prote outer membrane lip hypothetical prote penicillin-binding hypothetical prote hypothetical prote hypothetical prote hypothetical prote
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A; Residues: 1-409 < COS>
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Best Local Similarity
Matches 90; Conserv
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Result

Minimum Maximum

Searched:

Database

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A81315	Н90083	A90428	E86626	I40589	T25421	S22768	T45691	F70028	833921	S62460	D81746	S77508	B86210	E64559	H70203	
probable MCP-type	polyadenylate-bind	serine proteinase,	transcription-repa	parasporal crystal	hypothetical prote	130K protein - mai	receptor-like prot	transmembrane rece	alpha-amylase (EC	hypothetical prote	type III secretion	srrA protein - Syn	protein F22G5.6 [i	outer membrane pro	isoleucine-tRNA li	

ALIGNMENTS

C;Keywords: transferase F;1-30/Domain: signal sequence #status predicted <SIG> F;31-409/Product: thiamin pyridinylase #status predict A;Cross-references: EMBL:U17168; NID:g984284; A;Experimental source: strain 168 C;Complex: monomer [validated, MUID:96216437] A;Description: EC 2.5.1.2 [validated, MUID:96216437] A;Status: preliminary; translated from GB/EMBL/DDBJ 278 AVEVIKNILITNTLVLDLLGLGL------TLPANKNGIAHLAKSSNFYAQLSQ 323 LDSIFLSHFVDAGYLLPFGSQDIDQA-----EDVLPFALQGAKRNGEVYGLPQILCTNL 146 TLTVGLFPYLPSWNENGNEVKLINLIKDVLPTQVSGYNIEYTEFDCYSDASLQSLPDVFS --ELAKKLANVMASADTVEQALRPQADGQYPQYLLPARHQVYEALMQDYPIYSELAQ 368 --ALIDVTGQYTEYDLLPPLDPLNDKVIRGLRLLINMAGEKPSQYVPEDGDAYVRASWFA 255 SSAAVDIKAS----DLPQSGDQVNKDITQKYRTILDST-----VVASQREYINSVKQG LLSSPNGTQ--QASSLLELAQKVG---YEQIVYPD----VASSSSFTVFGLYQQLLQSS 171 TDSIFLPYLVSLG-----GVKSLDESLVRGVTGDLHSFVSSSASVNGSVYGFPQYLCSNF 121 TLKVAIYPYVP-----DPARFQAAVLDQWQRQEPGVKLEFTDWDSYSADPPDDL-DVFV 92 KPISNYYVGYSESMCEIKDIIRDQQYNVQLIGTS---DKPYVYTDVLALNSNLCDEKQKV 277 LFYRKGDLKIGQVDNIYELYKKIGTSHSEQIPPPQNKGLLINMAGGTTKASMYLE-----QGSGRAFIGYSESMMRMGDYA--EQVRFKPISSSAGQDIPLFYSDVVSVNSKTAHP----12.8%; Score 230; DE 25.2%; Pred. No. 1.1e cive 53; Mismatches DB 2; ..1e-08; PIDN:AAC44156.1; PID:g833806 predicted <MAT> 146; Length 409; Indels 68; Gaps 220 201 99 14;

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hypothetical protein T8K14.1 [imported] - Arabidopsis thaliana
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C.Accession: B96827
R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
A.; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, S.X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.; Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                 phycobilisome linker protein apcE - red alga (Porphyra purpurea) chloroplast C;Species: chloroplast Porphyra purpurea C;Cate: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 10-Sep-1997 C;Accession: S73184 R;Reith, M.; Munbolland, J. Plant Mol. Biol. Rep. 13, 333-335, 1995 A;Title: Complete nucleotide sequence of the Porphyra purpurea chloroplast g
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                     A; Accession: S73184
A; Status: preliminary;
A,Molecule
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Matches 75
                                                                  ;Reference number: S73108
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Residues: 1-1248 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DESIVR--GVTGDLHSFVSSSASVNGSVYGFPQYLCS--NFLLSSPNGTQ-----QASSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MNYNTGYMELRGLIGISHTGSECASDVSRFSTVENGTSDIERTNSSLHEFGNKLNHVQSA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GYNIEYTEF-----DCYSDASLQS-----LPDVFSTDSIFLPYLVSLGGVKSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIIRDQQYNVQLIGTSDKPYVYTDVLALNSNLCDEKQKVAVEVIKNLLTNTLVLDLLGLG 298
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Pred. No. 6.
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A;Residues: 1-886 <REI>A;Cross-references: EMBL:
A;Note: the nucleotide st
C;Genetics:
A;Genee: apcE
A;Genee: chloroplast
C;Keywords: chloroplast
                                                                                                                                                                                                                                                                                                                                                      R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redcarrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
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A; Residues: 1-613 < KUR>
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A; Accession: B90294
                                                                                                                                                                                                                                                                                                                                          A; Description: Sulfolobus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDASLQSLPDVFSTDSIFLPYLVSLG-GVKSLDESLVRGVTGDL-----HSFVS--SS 103
ATYKNIAIIIISYKDĖSKY-NITLSQYPSHILQGTDGIGL-FIIPLQALPWVYGKSVNSS
                               -----IEYTEFDCYSDASLQSLPD--VFSTDSIFLPYLVSLGGV-----KSLDES
                                                                 YPYNQVMFNYPENGPLELNMSYDNWSIHEISFIALPTVDVYPTKI--YNSSLYLGKGLLS
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                                                                                                                                                    19.5%;
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20.5%; Pred. No. 4.3;
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                                                                                                                                      72;
                                                                                                                                    Score 111.5;
Pred. No. 4.7;
72; Mismatches
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A;Status preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-2670 <CON>
A;Residues: 1-2670 <CON>
A;Cross-references: EMBL:Z68198; PIDN:CAA92385.1; GSPDB:GN00066; SPDB:SPAC18G6.05c
A;Experimental source: strain 972h-; cosmid c18G6
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C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change
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Matches 77; Conserv
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                                EILKNTSSPVPHIRESFISLLIYLPATFGSRFQPYLARAIPPILSGLADDSELVQTASLR 1781
                                                                                                                                          AKALGSLIEKLGEKKFPTLIPELFNVLRSECSEVDRQGAAQGLSEILAGLGLARLEDVLP
                                                                                                                                                                                                                                                       PILKYGLRERNAGTKROSAKIFGLMASLTEPENLAVYLESLMPRLREVLIDPVPDTRATA 1661
                                                                                                                                                                                                                                                                                                                                                                       ANKSLLRFGDVISNPEIQTLVPTLLKALSDCTRYTDDALEALLKTSFVHYLDPPSLALVI 160:
                                                                                                                                                                                                                                                                                                                                                                                                                               ASVN----GSVYGFP--QYLCSNFLLSSPNGTQQASSLLELAQKVGYEQIVYPDV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EYTEFDCYSDASLQSLPDVFSTD--SIFLPYLVSLGGVKSLDESLVRGVTGDLHSFVSSS 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GIASSASAPTFESQL
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                                                                                                                                                                                               LPQSGDQVNKDITQKYRTILDS--TVVASQREYINSVKQGKPISNYYVGYSESMCE--IK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EYNWRSKKASVEILGLMSYMAPKQLSVFLPTI----IPKLSEVLT-----DSHSQVRNT 1541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TQKYRTILDSTVVASQREYINSVKQGKPISNYY------VGYSESMCEIKDIIRD--QQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                            -ASSSSFTVFGLYQQLLQSSSSAAV------DIKASD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --YPDVASSSSTTVFGLYQQLLQSSSSAAVDIKASDLPQSGDQVNKDI 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.2%; Score 111.5;
19.7%; Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       483
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                                                                                  -YNVQLIGTSDKPYVYTDVLALNSNLCDEK---QKVAVE 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 107;
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                                                                                                                        R,Du, Z.; Le, T.T.
R,Du, Z.; Le, T.T.
Submitted to the EMBL Data Library, December submitted to the EMBL Data Library, Data Library, Data Library, Data Libr
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                                                                               A;Description: The sequence
A;Reference number: Z21225
A;Accession: T32787
                                                                                                                                                                                                                      C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change
                                                                                                                                                                                                                                                                              hypothetical protein F14D2.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans
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A;Experimental source: cv. Victory; root; 4 days old
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-448 <CRU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description: actin-bundling; Superfamily: plastin; alpha-actinin actin-binding domain homology; Keywords: actin binding; EF hand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 AYAYLLKALAPE-TSPETTLETKNPDERAKMVLEQAEKLDCKRYLTPKDITEGSANLNLA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            341 ---LNWANSKVK 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 LYQQLLQSSSSAAVDIKASDLPQSGDQVNKDITQK---YRTILDSTVVASQREYINSVKQ 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRCVDFANKEVK 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELKFSLVNLAGNDIVQGNKKLIVALLWQLMRFNILQLLNRLRSHSKGSQGKQITDADI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EV---IKNLLTNTLVL--DLLGLGLTLPANKNGIAHLAKSSNFYAQLSQQFDAKESEVRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --DVRNGWV-----LLEVLDKVSPGSVNWKL---ESKPPIKLPFRKLEN--CNQVVKIGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPDVFS--TDSIFLPYLVSLGGVKSLDESLVR-----GVTGDLHSFVSSSASVNGS
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Pred. No. 4.4;
                                                       from GB/EMBL/DDBJ
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A;Experimental source: strain Bristol N2; clone F14D2
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F53F4.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 21-Jan-2000 C;Accession: T22583
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Matches 59
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;Accession: T22583
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                                                                                                                                             ALANLLCAGYITITEDIDTFTENSVIVKGGREFKCDIFLTCTGYTFGFP
                                                                                                                                                                                                                    SLDESLVRG----VTGDLHSFVSSSASVNGS-----
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                                                                  PNGTQQASSLLELA-QKVGYEQIVYPDVASSSSFTVFGLYQQL-----LQSSSSAAV 176
                                                                                                                                                                                                                                                                                       YDVQL--FSRYYDTLLKTIPHAVAND--FMEYRLQQRMDHDVYGLRPDHRFFQQHPTVND 293
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                                                                                                                                                                                                                                                                                                                                                             YNIEYTEFDCYSDASLQSLPDVFSTDSIFLPYLV-----SLGGVK-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 59; Conserv
-DSDIVEIKNÓQVPLYKYVFP---PNSDSVAVIGLIQPIGSIAPISEIQSRWAARV
                                                                                                                                                                                                                                                                                                                                                                                                                                6.0%; Score 108; DB llarity 21.7%; Pred. No. 6.6; Conservative 47; Mismatches
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R;Apt, K.E.; Grossman, A.R. submitted to the EMBL Data Library, A;Description: Characterization and
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A;Genome: ch
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A; Residues: 1-885 < APT>
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                                                                                QQFDAKESEVRV
                                                                                                                 LASQGLSSFIT---VLVNSNEYNQVFGVNIVPYRRFTTLPA----ANFPNTEKLYNTLT
                                                                                                                                                VAVEVIKNLLTNTLVL---
                                                                                                                                                                                  LVNNNITVQQF-IEQIGSSSLYGREFYQPYPNTKVIELGTKHFLGRAPNNQAEIRYYNQI
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                                                                                                                                                                                                                 -IKDIIRDQQYNVQLIGTSD------KPYVYTDVLALN-----SNLCDEK---QK 276
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                                                KQ----SSEIIV
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                                                 875
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                                                                                                                                                  -DLLGLGL----
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d transcript
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C;Accession: A96714
R;Theologis, A.; Ecker, J.R.; Palm, C.
Chin, C.W.; Chung, M.K.; Conn, L.; Cc
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu,

C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.

#text_change 31-Mar-2001

Johnson-Hopson, C.; Khan, S.; S.X.; Liu, Z.A.; Luros, J.S.;

Khaykin, E.; Kim, C Maiti, R.; Marziali A96714
hypothetical protein T6L1.12 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_chango

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A; Molecule type: DNA
A; Molecule type: DNA
A; Mesidues: 1-2819 <KUR>
A; Residues: 1-2819 <KUR>
A; Cross-references: GB: AL445566; PID: g14089727; PIDN: CAC13486.1; GSPDB: GN00153
A; Cross-references: GB: AL445566; PID: g14089727; PIDN: CAC13486.1; GSPDB: GN00153
                                                                                                                                                                                                  R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; (Nucleic Acids Res. 29, 2145-2153, 2001

A;Title: The complete genome sequence of the murine respiratory A;Reference number: A99512; MUID:21267165; PMID:11353084

A;Accession: A99551
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A90551
                                                                                                                                                                                                                                                                                                                  conserved hypothetical protein MYPU_3130 [imported] - Mycoplasma pulmonis (strain C;Species: Mycoplasma pulmonis C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
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A; Residues: 1-1033 <STO>
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A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A96714
                                                                                                                                                                                        A; Status: preliminary
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Pred. No. 24;
Score
Pred.
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No.
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1.1e+02;
                                                                                                                                                                                                                                                                                 V.; Samson, D.; Galisson, F.; Moszer,
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submitted to the EMBL Data Library, July submitted to the Part Data Library, July submitted to the EMBL Data Library submitted to the EMBL Da
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A;Molecule type: DNA
A;Residues: 1-545 <KAW>
A;Cross-references: GB;AJ248283; GB:AL096836; NID:g5457433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A75001
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Best Local
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                                                                                                                                                                                                                                                                                                             19 WNENGNEVKLINLIKDVLPTQVSGYNIEYTEFDCYSDASLQSLPDVFSTDSIFLPYLVSL
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IRKDVAKCVGLDVSTLPDKVKNGEFTWSDVYE
                                                             ---ELAOKVGYEQIVYPDVASSSSTVFGLYQ 165
                                                                                                                           GYILDITDYAKAYQSVLNDFYPSLLEAAKYKGRLYGLPQ-
                                                                                                                                                                                        GGVKSLDE--SLVRGVTGDLHSFVSSSASVNGSVYGFPQYLCSNFLLSSPNGTQQASSLL 136
                                                                                                                                                                                                                                                WKENGINVKIV-IPEDMIRYDQS-FKDQYQEF--LSKQPLGQAGDFFVNSYAFLPNLAEE 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEFSTFMKKSI 1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NKNKYLAYENLNDFLIDALVDNKENIINLSSNTLGKIKTDDEFKNIIKSFITKNLMTSDS
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RESULT 13
682934
hypothetical protein UU094 [imported] - Ureaplasma C;Species: Ureaplasma urealyticum C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 C;Accession: G82934

urealyticum #text_change

20-Aug-2000

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein lin2511 [imported] - Listeria innocua (strain Clip11262) C;Species: Listeria innocua
C;Species: Listeria innocua
C, te: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C, te: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C, tession: AB1746
E, bession: AB1746
E, Duchaud, E.; Durand, A.; Baquero, F.; Berche, P.;
Cominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; F
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A;Residues: 1-1054 <GLA>
A;Cross-references: GB:AE002109; GB:AF222894; NID:g6899045; PIDN:AAF30500.1; GSPDB:GN00:A;Experimental source: serovar 3; biovar 1
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                                                                                                                                                                                                                                                                                                      Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, JA; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: AB1746
A; Status: preliminary
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                                                                                                                                                                                                                        A;Cross-references: GB:AL592022; PIDN:CAC97738.1; PID:g16415033; GSPDB:GN00178 A;Experimental source: strain Clip11262
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A;Residues: 1-358 <GLA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Status: preliminary
                                                                                                                       Query Match
Best Local
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jones, L.M.; Karst,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                809
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                     53
                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             госат
                  SDNYIKKLGSDIDLNQLKKSNIQYKISVDSDSSSSYSAYSLHWKGKEPLDLTLHALQNSE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IST-NYFLTKIKILDLISL-----NKNDQLDYHKGVEMIFSLLKKF 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAQKVG-----YEQIVY--PDVASSSSFTVFGLYQQLLQSSSSAAVDIKASDLPQS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VKSLDESLVRGVTGDLH---SFVSSSASVNGSVYGFPQYLCSNFLLSSPNGTQQASSLLE 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NELKKLNEQQILKDIEYAFTSGY-----DVAIDSIGSIF-
                                                        SPNGTQQASSLLELAQ--KVGYEQIVYPDVASSSSFTVFGLYQQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEVIKNLLTNTLVLDLLGLGLTLPANKNGIAHLAKSSNFYAQLSQQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DELFSFFLNLKQNDLPSSINFKIGDQNYTLYDLITEVKK--IANNLIPHENQYDPKDQQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CEI-----KDI-----IRDQQYNVQLIGTSDKPYVYTDVLALNSNLCDEKQKVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNOSLGMVIDGFKPILKEIIYNNPSIDQSVKNTIW-----SKIDSMDFKNNLIAEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDQVNKDITQKYRTILDS---TVVASQREYINSV-----KQGKPISNYYVGYSESM
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                                                                                                  62; Conservative
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                                                                                                5.9%; Score 105.5;
20.9%; Pred. No. 5.5,
tive 44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.9%; Score 106; DB 20.2%; Pred. No. 26; tive 51; Mismatches
                                                                                                                     5
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                                                                                                                                        Length
                                                          -----LLQSSS 172
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                                                                                                                                             358;
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J.A.;
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H.; Wehland
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                                                                                                  13;
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Fsihi, H.
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R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586, 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-1277 <KLE>
A;Cross-references: GB:AE000785; NID:g2689951; PIDN:AAC66031.1; PID:g2689960; TIGR:BBB0
A;Experimental source: strain B31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; nucleic acid A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete,
A;Reference number: A70100; MUID:98065943; PMID:9403685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein BBE02 - Lyme disease spirochete plasmid E/lp25
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                      VLDLLGLGLTLPANKNGIAHLAKSSNFYAQLSQQF----DAKES 330
                                                                           SIIEFKD---NEEFT--LINK----MFSKFSALGEGYIDFKKGLDPSIKNRKSLLKE--
                                                                                                                SMCEIKDIIRDQQYNVQLIGTSDKPYVYTDVLALNSNLCDEKQKV--AVEVIKNLLTNTL
                                                                                                                                                         S----FKAKFMIQSSDNILKEITRDLKDSKDDAYKGIELN-INQIKKLSPI-----QE
                                                                                                                                                                                          SAAVDIKASDLPQSGDQVNKDITQKYRTILDSTVVASQREYINSVKQGKPISNYYVGYSE
                                                                                                                                                                                                                                     FARYKL-NYIYQFENKKR---
                                                                                                                                                                                                                                                                          FPQYLCSNFLLSSPNGTQQASSLLELAQKVGYEQIVYPDVASSSSFTVFGLYQQLLQSSS
                                                                                                                                                                                                                                                                                                                 -----DPNLFRYFVTF-NLKLIKEK-----GNL-TYLVPSAIWNESSSRILRKHI 883
                                                                                                                                                                                                                                                                                                                                                          QSLPDVFSTDSIFLPYLVSLGGVKSLDESLVRGVTGDLHSFVSSSASVNGS-----VYG
                                                                                                                                                                                                                                                                                                                                                                                                 HIPNYRKLG--IKEQNIIKQEILSKDNHPLSIEYNEEKNSIIAINNIYKFDFKCFTSGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVLDLLGLGLTL-PANKNGIAHLAKSSNFYAQLSQQFDAKESE-VRVLRCVDFANKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STVVASQREYINSVKQGKPISNY-YVGYSE------SMCEIKDIIRDQQY 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity 22.1
76; Conservative
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CNNKNLIFLYSGANIH-QFNSRFFEDKDAKES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 105.5;
Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                       -FKDVHSSFKFAIFQL-SNIKESTS
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1050
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Whit Vugt

Search completed: January

24,

2003,

19:43:11

Job time : 28

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Minimum
Maximum
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Maximum Match 100%
Listing first 45 s
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            number of hits satisfying chosen parameters:
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80
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seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                             Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-989-735-194
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US-09-991-181-194
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US-09-989-734-194
US-09-989-731-194
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US-09-989-723-194
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US-09-951-402-3
US-09-951-401-3
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Sequence 6, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 194, App
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Sequence 13865, A	•	`	Sequence 180, App	Sequence 4937, Ap	-	Sequence 5834, Ap	Sequence 4306, Ap	m	Sequence 206, App		e !:	Sequence 11, Appl	Sequence 80, Appl		မ္တ	5	Sequence 565, App	Sequence 16, Appl	19	19	Sequence 194, App	Sequence 194, App	19	19	Sequence 194, App

ALIGNMENTS

RESULT 1 US-08-834-666A-6

Sequence 6, Application US/08834666A Patent No. US20020044949A1

GENERAL INFORMATION:
APPLICANT: Kleanth
APPLICANT: Lissolo
APPLICANT: Tomb, J.
APPLICANT: Miller,
APPLICANT: Al-Gara

Lissolo, Ling Tomb, Jean-Francois Miller, Charles

Kleanthous,

Harold

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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,666A
FILING DATE: 01-APR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 06132/038001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                         TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Al-Garawi, Amal
TITLE OF INVENTION: 76 kDa Helicobacter Polypeptides and
TITLE OF INVENTION: Corresponding Polynucleotide Molecules
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U
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STRANDEDNESS:
                TYPE: amino acids
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SEQ ID NO 3
LENGTH: 2037
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                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/951,402
CURRENT FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: US 09/306,998
PRIOR FILING DATE: 1999-05-07
RIOR APPLICATION NUMBER: US 60/084,740
NOR FILING DATE: 1998-05-08
UMBER OF SEQ ID NOS: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bartel, Paul L.
APPLICANT: Tavtigian, Sean V.
TITLE OF INVENTION: MMSC2- An MMAC1 Interacting
FILE REFERENCE: MMSC2
                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 SGDQVNKDITQKYRTILDSTVVASQREYINSVKQGKPISNYY-VGYSESMCEIKDIIRDQ 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 SASVNGSVYGFPQYLCSNFLLSSPNG-------
                                  127 NGTQQASSLLELAQKVGYEQIVYPDVASSSSFTVFGLY------QQLLQSSSSAAVDI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Signal Sequence LOCATION: 1...20 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity nes 63; Conserv
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                                                                                                                                                                                                                      Local Similarity 21.4 nes 75; Conservative
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 DGLNYGSSLPSSPPK---
                                                                                                          TDSIFLPYLVSLGGVKSLDESLVRGVTGDLHSFVSSSASVNGSVYGFPQYLCSNFLLSSP 126
                                                                                                                                                                              TLTVGLFPYLPSWNENGNEVKLINLIKDVLPTQVSGYNIEYTEFDCYSDASLQSLPDVFS 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QYNVQLIGTSDKPYVYTDVLALNSNLCDE-----KQKVAVEVIKNLL----
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internal
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21.1%; Pred. No. 1.6
                                                                                                                                                                                                                  5.4%; Score 97.5; DB 9;
21.4%; Pred. No. 11;
ative 48; Mismatches 147;
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-- DVIENSCDPVLDLHMSLEELYTQNLLQRQDENTPSV 919
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CURRENT FILING DATE: 2001-09-14

PRIOR APPLICATION NUMBER: US 09/306,998

PRIOR FILING DATE: 1999-05-07

PRIOR APPLICATION NUMBER: US 60/084,740

PRIOR FILING DATE: 1998-05-08

NUMBER OF SEQ ID NOS: 72

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3

LENGTH: 2037

TYPE: PRT

ORGANISM: Homo sapiens

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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CURRENT FILING DATE: 2001-09-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bartel, Paul L.
APPLICANT: Tavtigian, Sean V.
TITLE OF INVENTION: MMSC2- An MMAC1 Interacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: MMSC2
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1015 NSSLGMTVSANKDGLGMIVRSIIHGGAIS-----RDGRIAIGDCILSINEE
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                                        294 LLGLGLTLPANKNGIAHLAKSSNFYAQLSQQFDAKESEVRVLRCVDFANKE 344
                                                                                                          234 MCEIKDIIRDQQYNVQLIGTSDKPYVYTDVLALNSNLCDEKQKVAVEVIKNLLTNTLVLD 293
                                                                                                                                                                         920 DISMGPASGFTINDYTPANAIEQQYE--CENTIVWTESHLPSEV-----IS
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                                                                                        SAELPSVLPDS---
                                                                                                                                                                                                                    KASDLPQSGDQVN-----KDITQKYRTILDSTVVASQREYINSVKQGKPISNYYVGYSES
                                                                                                                                                                                                                                                                 DGLNYGSSLPSSPPK-----DVIENSCDPVLDLHMSLEELYTQNLLQRQDENTPSV 919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.4%; Score 97.5; DB 10; ilarity 21.4%; Pred. No. 11; Conservative 48; Mismatches 147;
                                                                                        ---AGKGSEYLLEQSSLACNAE-CVMLQNVSKESFER--TINIAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
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US-09-922-101-3

Sequence 3, Application US/09922101 Patent No. US20020146711A1 GENERAL INFORMATION:

APPLICANT: Bartel, Paul L. APPLICANT: Tavtigian, Sean V. TITLE OF INVENTION: MMSC2- An

MMAC1 Interacting Protein

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; LENGTH: 2037
; TYPE: PRT
; ORGANISM: Homo s
US-09-922-101-3
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CURRENT APPLICATION NUMBER: US/09/922,101
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/306,998
PRIOR FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 2037
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PLICANT: Baker, Kevin P.
PLICANT: Botstein, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 NGTQQASSLLELAQKVGYEQIVYPDVASSSSFTVFGLY------QQLLQSSSSAAVDI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 TDSIFLPYLVSLGGVKSLDESLVRGVTGDLHSFVSSSASVNGSVYGFPQYLCSNFLLSSP 126
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   INVENTION:
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Roy, Margaret Ann
Stewart, Timothy A.
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Godowski, Paul J.
Grimaldi, J. Christopher
                                              Watanabe, Colin K. Williams, P. Mickey Wood, William I.
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                                                                                                                                                                                                 Gurney, Austin L
Kljavin, Ivar J.
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Pred. No. 11;
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CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
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PRIOR FILING DATE: 1997-06-16
OR PELICATION NUMBER: 60/088742
OR FILING DATE: 1998-06-10
OR PELICATION NUMBER: 60/088810
OR APPLICATION NUMBER: 60/088824
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088826
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088826
OR FILING DATE: 1998-06-11
OR APPLICATION NUMBER: 60/088658
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OR FILING DATE: 1998-06-03
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OR APPLICATION NUMBER: 60/088025
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OR APPLICATION NUMBER: 60/088026
OR APPLICATION NUMBER: 60/088026
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/08028
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PREPLICATION NUMBER: 60/078910
DR FILING DATE: 1998-03-20
DR PILICATION NUMBER: 60/083322
DR FILING DATE: 1998-04-28
DR APPLICATION NUMBER: 60/084600
DR FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/087607
FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087609
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FILING DATE: 1997-11-12
APPLICATION NUMBER: 60/065311
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088033
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APPLICATION NUMBER: 60/088212
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FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/075945
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APPLICATION NUMBER: 60/066770
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60/089512 60/089440

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APPLICATION NUMBER: 60/089598 FILING DATE: 1998-06-17

APPLICATION NUMBER: 60/089600 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089653 FILING DATE: 1998-06-17

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RESULT 6
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OR APPLICATION NUMBER: 60/090696
OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/090862
OR FILING DATE: 1998-06-26
OR FILING DATE: 1998-06-26
OR APPLICATION NUMBER: 60/091863
OR FILING DATE: 1998-07-01
OR APPLICATION NUMBER: 60/091478
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/09154
OR APPLICATION NUMBER: 60/091519
OR APPLICATION NUMBER: 60/091519
OR APPLICATION NUMBER: 60/091626
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091633
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091978
OR APPLICATION NUMBER: 60/091982
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OR APPLICATION NUMBER: 60/091982
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Baker, Kevin P.
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Fong, Sherman
Gerber, Hanspeter
Gerritsen, Mary E.
                                                 Gurney, Austin
Kljavin, Ivar J
                                                                                Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
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 Paoni, Nicholas
                               Napier, Mary
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2.3;
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APPLICATION NUMBER: 60/089801 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089907 FILING DATE: 1998-06-18

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CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-66-16
PRIOR PPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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Stewart, Timothy A.
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FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089947
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GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
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APPLICATION NUMBER: 60/091633
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CURRENT FILING DATE: 2001-11-19
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OR FILING DATE: 1998-06-02
OR APPLICATION NUMBER: 60/087759
OR APPLICATION NUMBER: 60/087827
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OR APPLICATION NUMBER: 60/088021
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RAPPLICATION NUMBER: 60/084600

OR FILING DATE: 1998-05-07

OR APPLICATION NUMBER: 60/087106

OR FILING DATE: 1998-05-28

OR APPLICATION NUMBER: 60/087607

OR FILING DATE: 1998-06-02
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APPLICATION NUMBER: 60/062250
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APPLICATION NUMBER: 60/083322
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Goddard, Audrey
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Kljavin, Ivar J.
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art, Timothy A.
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NUMBER: 60/092182
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RESULT 8 US-09-990-444-194 ; Sequence 194, Application US/09990444 ; Publication No. US20020193300A1

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368 339 308 289 253 236 204 177 38;

Gaps

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FILE REFERENCE: P2730DTC19
CURRENT APPLICATION NUMBER: US/09/990,444
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
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PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR APPLICATION NUMBER: 60/08760
PRIOR FILING DATE: 1998-05-07
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PRIOR APPLICATION NUMBER: 60/087827
PRIOR APPLICATION NUMBER: 60/088021
PRIOR APPLICATION NUMBER: 60/088029
PRIOR PRILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
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Williams, P. Mickey
Wood, William I.
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
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Kljavin, Ivar C
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Botstein, David
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, Margaret Ann
wart, Timothy A
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OR APPLICATION NUMBER: 60/088810
OR FILING DATE: 1998-06-10
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OR APPLICATION NUMBER: 60/088861
OR APPLICATION NUMBER: 60/088861
OR APPLICATION NUMBER: 60/089866
OR FILING DATE: 1998-06-12
OR APPLICATION NUMBER: 60/089105
OR FILING DATE: 1998-06-16
OR APPLICATION NUMBER: 60/089512
OR APPLICATION NUMBER: 60/089512
OR FILING DATE: 1998-06-16
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OR APPLICATION NUMBER: 60/089538
OR FILING DATE: 1998-06-17
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OR APPLICATION NUMBER: 60/089901
OR APPLICATION NUMBER: 60/089908
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APPLICATION NUMBER: 60/088212
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APPLICATION NUMBER: 60/088167
FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088202
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R APPLICATION NUMBER: 6
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FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/092182
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FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091978
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APPLICATION NUMBER: 60/990862
FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/090863
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APPLICATION NUMBER: 60/090695
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APPLICATION NUMBER: 60/090696
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APPLICATION NUMBER: 60/091626
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APPLICATION NUMBER: 60/091519
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APPLICATION NUMBER: 60/090690
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APPLICATION NUMBER: 60/090445
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LYHCLGSVAGTMMCLMYGATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPD
                                LVLDLLGLGLTLPANKNGIAHLAKSSNFYAQLSQQFDAKESE-----VRVLRCVD 339
                                                                                                    IKDIIRDQQYNVQLI-GTSDKPYVYT---DVLALNSNLCDEKQKV---AVEVIKNLLTNT 289
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                                                            NUMBER: 60/090535
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Pred. No. 2.
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CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065186
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PRIOR FILING DATE: 1997-11-12
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PLICANT: Botstein, David
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Tumas, D
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Wood, William
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Godowski, Paul J.
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Gerritsen, Mary E.
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                                             NUMBER: 60/087609
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                                                                OR FILING DATE: 1998-06-16
OR APPLICATION NUMBER: 60/089532
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Query Match 5.4%; Score 97; DB 9; Length 615; Best Local Similarity 21.3%; Pred. No. 2.3;
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GENERAL INFORMATION:
APPLICANT: Babkenazi, Avi J.
APPLICANT: Babker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Forg, Sherman
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088738
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APPLICATION NUMBER: 60/088029
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APPLICATION NUMBER: 60/088030
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APPLICATION NUMBER: 60/087759
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APPLICATION NUMBER: 60/087609
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FILING DATE: 1998-05-28
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APPLICATION NUMBER: 60/066770
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APPLICATION NUMBER: 60/088033
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APPLICATION NUMBER: 60/089512
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APPLICATION NUMBER: 60/089801
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APPLICATION NUMBER: 60/089908
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APPLICATION NUMBER: 60/090252
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OR APPLICATION NUMBER: 60/091544
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OR APPLICATION NUMBER: 60/091978
OR APPLICATION NUMBER: 60/091978
OR FILING DATE: 1998-07-07
OR APPLICATION NUMBER: 60/091982
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OR FILING DATE: 1998-07-09
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54; Conservative
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Baker, Kevin P.
                                                        Watanabe, Colin K. Williams, P. Mickey Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Grimaldi,J.Christopher
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Kljavin, Ivar J.
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CURRENT APPLICATION NUMBER: US/09/989,734
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR PPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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APPLICATION NUMBER: 60/091360
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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J
Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
                   Paoni
                                          Pan, James
                                                       Napier, Mary A.
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Ferrara, Napoleone
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CURRENT FILING DATE: 2001-11-15
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OR APPLICATION NUMBER: 60/088021
OR APPLICATION NUMBER: 60/088025
OR FILING DATE: 1998-06-04
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OR APPLICATION NUMBER: 60/062250
OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/065186
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OR FILING DATE: 1998-04-28

OR APPLICATION NUMBER: 60/084600

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OR APPLICATION NUMBER: 60/087106

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RESULT 3
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                                      Sequence 2, Application US/07915203
PATENT NO. 5359048
GENERAL INFORMATION:
APPLICANT: Obba, Michio
APPLICANT: Iwahana, Hidenori
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LENGTH: 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4104, Application US/09134001C Patent No. 6380370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/134,001C
URRENT FILING DATE: 1998-08-13
FIGR APPLICATION NUMBER: US 60/064,964
FRIOR FILING DATE: 1997-11-08
FRIOR APPLICATION NUMBER: US 60/055,779
FRIOR FILING DATE: 1997-08-14
FRIOR FILING DATE: 1997-08-14
FRIOR FILING DATE: 1997-08-14
FRIOR FILING DATE: 1997-08-14
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      APPLICANT:
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                                                                                                                                                                                                                                   -VSELAKRIDLTTQHYNELDHI----IENSKDTLKQF
                                                                                                                                                                                                                                                                          FYAQLSQQFDAKESEVRVLRCVDFANKEVKNCAGVLRPF 355
                                                                                                                                                                                                                                                                                                                                                                                                                             NYYVGYS---ESMCEIKDIIRDQQYNVQLIGTSDKP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E---KKMIKAIRHTKTDVLVGTRASFNI-----LISKYAKAEIVTIAMEHMNFDAHPDQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYNDLNIIENNEVFYAMKSFTFFMHNIYAMGGTVKSVTQLANTLAEKGHPVTIISVFRGA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSPYFELHSAIKVKVVVDYRLKLKNTRAITANRIKKYTPFLNTKVISQFEPGKSQFSSYV 120
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Iwahana, Hidenori
Sato, Reiichi
Suzuki, No. 53590
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    5359048ukazu
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Pred. No. 0.14;
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Best Local Similarity 22.6%;
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/I
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT:
APPLICANT:
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ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
1046 VQQLSDTSVLVIPNWNSQVSQQFTVQPNYRYVLRVT--ARKE 1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
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CTTY: Gainesville
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                 IPGMNYTSFTE
                                                                                                   --ALNSNLCDEKQKVAVEVIKNLLTNTL--VLDLLGLGLTLPAN--KNGIAHLAKSS---
                                                                                                                                     KTYY-AAKQA--IDRLFADYQDQKLNSGVEMSDLLAAQNL-VQSI-----PYVYNDALPE
                                                                                                                                                                    REYINSVKQGKPISNYYVGYSE----SMCEIKDIIRDQQYNVQLIGTSDKPYVYTDVL--
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VENTION: No. 5359048el Microorganism and Insecticide
EQUENCES: 2
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Sakanaka, Kazunobu
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                              NFYAQLSQQFDAKESEVRVLRCVDFANKE 344
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Pred. No. 2.3;
58; Mismatches
                                                                 LTNRLQQAWNLYDLQNAIPNGDFRNGLSNWNATSDVN 1045
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RESULT 4 US-08-272-887-2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/272,887
FILING DATE: 08-JUL-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA: 407/915,203
FILING DATE: 23-JUL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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LENGTH: 1149 amino aci
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CORRESPONDENCE ADDRESS:
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t Local Similarity 22.6%;
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 265
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                                                                   211 REYINSVKQGKPISNYYVGYSE----SMCEIKDIIRDQQYNVQLIGTSDKPYVYTDVL--
                                                                                                                                         153 ASSSSFTVFGLYQQLLQSSSSAAVDIKASDLPQSGDQVN--KDITQKYRTILDSTVVASQ 210
                                                                                                                                                                                                                                                 786 ----YQQIDESLLKPYTRYKLKGFIGSSQDLEIKLIRHRANQIVKNVPDNLLPDVRPVNS 841
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REGISTRATION NUMBER: 31,79
                                                                                                                                                                                                                                                                                                                                                             26 VKLINLIKDVLPTQVSGYN-----IEYTEFD-CYSDASLQSLPDVFSTDSIFLP-YLV 76
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--ALNSNLCDEKQKVAVEVIKNLLTNTL--VLDLLGLGLTLPAN--KNGIAHLAKSS---
                                                                                                                                                                             CGGVDRCSEQQYVDANLALENNGENGNMSSDSHAFSFHIDTGEIDLNENTGI-WIVFKIP 900
                                                                                                                                                                                                                                                                                       SLGGVKSLDESLVRGVTG-DLHSFVSSSASV-----NGSVYGFP------
                                KTYY-AAKQA--IDRLFADYQDQKLNSGVEMSDLLAAQNL-VQSI-----PYVYNDALPE
                                                                                                       TTNGNATLGNL--EFVEEG-----PLSGETLEWAQQQEQQWQDKMARKRAASE 946
                                                                                                                                                                                                               -----QYLCSNFLL--SSPNGTQQASS-----LLELAQKVGYEQIVYPDV 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T: Kawasugi, Tadaaki
INVENTION: No. 5747450el Microorganism and Insecticide
F SEQUENCES: 2
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2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1149 amino acids
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Sakanaka, Kazunobu
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Pred. No. 2.
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Mismatches 126; Indels 127;
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Parent No. 5824878
                                                                                                                                                                          Matches
                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                             TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1149 amino aci
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ATTORNEY/AGENT INFORMATION:
NAME: Sallwanchik, David R.
REGISTRATION NUMBER: 31,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kawasugi, Tadaaki
TITLE OF INVENTION: No. 5824878el Microorganism and Insecticide
NUMBER OF SEQUENCES: 2
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115
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                                                                                                   728 VQARNLLQDTGFNRINGENGWTGSTGIEVVEGDVLFKDRSLR-LTSAREIDTETYPTYL- 785
                                786 ----YQQIDESLLKPYTRYKLKGFIGSSQDLEIKLIRHRANQIVKNVPDNLLPDVRPVNS
                                                                   77
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                                                                                                                                    26 VKLINLIKDVLPTQVSGYN-----IEYTEFD-CYSDASLQSLPDVFSTDSIFLP-YLV 76
                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: M/K
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CLASSIFICATION: 435
                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                TYPE:
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                                                                   SLGGVKSLDESLVRGVTG-DLHSFVSSSASV-----
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Asano, Shouji
Asano, Tadaaki
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Sato, Reiichi
                                                                                                                                                                        Conservative
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-QYLCSNFLL--SSPNGTQQASS----
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                                                                                                                                                                                       Score 98.5;
Pred. No. 2
                                                                                                                                                                        Mismatches 126;
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---LLELAQKVGYEQIVYPDV 152
                                                                   -NGSVYGFP----- 114
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RESULT 7
US-09-134-001C-5661
Sequence 5661, Application US/09134001C
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Best Local Similarity
Matches 67; Conserva
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APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
APPLICANT: MACTIVER, ISOBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-336-447A-7
GENERAL
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Patent No. 6310190
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APPLICANT: EREDENBURG, ROSS A.
APPLICANT: EREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:024
CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Moraxella catarrhalis
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                                                                                                                                                                                                                                                             KQKVA-----VEVIKNLLTNTLVLDLLGLGLTLPAN-KNGIAHLAKSSNFYAQLSQQFDA 327
                                                                                                                                                                                                                                                                                                                                                                                   STDAVNGSQLY-----ALATAVDDNQYDIEINQDNI-KDL-QKEVKGLDKEVGYLSRD-
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  INFORMATION
                                                                                                                                        HSSDIKTLAKASAANTDRIAKNKA 448
                                                                                                                                                                                KESEVRVLRCVDFANKE--VKNCA 349
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                                                                                                                                                                                                                        QADIAKNQADIKTLENNVEEGL-LDLSGRLIDQKADIDNNINHI----
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US-09-540-824-26
Sequence 26, Application US/09540824
Patent No. 6383753
GENERAL INFORMATION:
APPLICANT: Thiele, Dennis
APPLICANT: Liu, Phillip
TITLE OF INVENTION: No. 6383753el Yeast and Mammalian Regulators of Cell Prolifera
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; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-09-540-824-26
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SEQ ID NO 5661
LENGTH: 639
TYPE: PRT
                                                                                                                                                                                                                                                                          SOFTWARE:
SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                        Matches
                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                             FILE REFERENCE: UM-04266
CURRENT APPLICATION NUMBER: US/09/540,824
CURRENT FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
PRIOR FILING DATE: 1997-08-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          381 PKEITVTSDKYIPNVSTKKGQTDIIIPRGS---LKDVVKTDKKRTAYVGSKKFRLKVSLR 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  325 EVILSSPHDVTLKNQKQAN---ELAFKLNNRNIEHYYNYKEVVYAKVYKDHLFSE-GVYR 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 NFILSSPN-----GTQQASSLLELAQKV------GYEQIVYPDVASSSSFTVFGLY- 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 SLPDVFSTDSIFLPYLVSLGGVKSLDESLVRGVTGDLHSFVSSSASVNGSVYGFPQYLCS 119
                                        24 NEVKLINLIKDV----LPTQVSGY-NIEYTEFDCYSDASLQSLPDVFSTDSIFLPYLVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVTDVMFTSPII--YRVKKNAFSLTVMTVVSAITVSVLCFAALSRST------------ITN 324
SHVEFVQLLKGLDYKDYPTVVSRIRTLHHVKLHPDNKSRLEN----FSV--ILLQHILHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---KQIDETEDELENYTILRKLGFTHQDM 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QLSQQFDAKESEVR---VLRCVDFANKEV 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YTDVLALNSNLCDEKQKVAVEVIKNLLTNTLVLDLLGLGLTLPANKNGIAHLAKSSNFYA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KGINKVYFMSDVDRGRPTLILN-----DEDYQKIREHIKEKNIVSQYGFDLKNKNDLPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EYIN-----SVKQGKP--ISNYYVGYSESMCEIKDIIRDQ----QYNVQLIGTSDKPYV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -QQLLQSSSSAAVDIKASD-----LPQSGDQVNKDI--TQKYRTILDST----VVASQR
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                                                                                        Conservative
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22.5%; Pred. No. 1.1;
ative 59; Mismatches
                                                                                   5.4%; Score 97.5; I
19.7%; Pred. No. 1.7;
tive 65; Mismatches
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                                                                                                                                  Length
                                                                                        Indels 135;
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                                                                                     Gaps
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  466
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APPLICANT: Battel, Paul L.

APPLICANT: Battel, Sen V.

APPLICANT: Tavtigian, Sen V.

TITLE OF INVENTION: MMSC2- An MMAC1 Interacting Profile Reference: MMSC2

CURRENT APPLICATION NUMBER: US/09/306,998

CURRENT FILING DATE: 1999-05-07

EARLIER APPLICATION NUMBER: US 60/084,740

EARLIER FILING DATE: 1998-05-08

NUMBER OF SEQ ID NOS: 72
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US-09-306-998-3
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SEQ ID NO 3
LENGTH: 2037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 5.4%; Score 97.5; DB 4; Length 2037; Best Local Similarity 21.4%; Pred. No. 7.2; Ches 75; Conservative 48; Mismatches 147; Indels 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09306998 Patent No. 6291173 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                    1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       778
                                                           294 LIGIGITLPANKNGIAHLAKSSNFYAQLSQQFDAKESEVRVLRCVDFANKE 344
                                                                                                                    964
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67
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                                                                                                             SAELPSVLPDS-----AGKGSEYLLEQSSLACNAE-CVMLQNVSKESFER--TINIAKG 1014
                                                                                                                                                                                                                                                                                                                                                                                                               ADLA----LVGTNDADLVDES-----TFESPYSPENDSIYSTQASILSLHGSSCG 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVRIGVAKPLPLSPEEG----YVSAKED-----SFLYPPHSC-EEAGLADKP-LFR 822
               NSSLGMTVSANKDGLGMIVRSIIHGGAIS-----RDGRIAIGDCILSINEE 1060
                                                                                                                                                           MCBIKDIIRDQQYNVQLIGTSDKPYVYTDVLALNSNLCDEKQKVAVEVIKNLLTNTLVLD 293
                                                                                                                                                                                                             DISMGPASGFTINDYTPANAIEQQYE--CENTIVWTESHLPSEV------IS
                                                                                                                                                                                                                                                                                                                    DGLNYGSSLPSSPPK--
                                                                                                                                                                                                                                                                                                                                                              NGTQQASSLLELAQKVGYEQIVYPDVASSSSFTVFGLY-----QQLLQSSSSAAVDI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TDSIFLPYLVSLGGVKSLDESLVRGVTGDLHSFVSSSASVNGSVYGFPQYLCSNFLLSSP 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLGITSQVPKFEEGYS-LDKSSHDIDPERAQLNKLRAQHRDAKKGAIRTLR 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -LGLT--LPANKNGIAHLAKSSNFY----AQL----SQQFDAKESEVRVLR 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQAFIEIFVPIMDMLQLYSLKKELLSKRLSEKLLSTLQAVSDSIESAKANRKPLALQSHR 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVCKKLYIANLFLKFQSYSHRYVPEVITAVSQALYLLYPNFISIVPGTFALPDSLKE--- 624
                                                                                                                                                                                                                                                                 KASDLPQSGDQVN-----KDITQKYRTILDSTVVASQREYINSVKQGKPISNYYVGYSES 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QKVAVEVI------KNLLTNTLVLDLLG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISNYYVGYSESMCEIKDIIRDQQYNVQLIGTSDKP--YVYTDVLALNSNLCDE-----K 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DITCK-----NSVKQGKP 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKSYVYPEIKFPEI---SDLLFFNLTGSIFPTSDKKHIVVSPVMLTMAESLSQSPADSLS 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQKVGYEQIVYPDVASSSSFTVFGLYQQLLQSSSSAAVDIK-----ASDLPQSGDQVNK 192
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                                                                                                                                                                                                                                                                                                               -----DVIENSCDPVLDLHMSLEELYTONLLORODENTPSV 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48; Mismatches 147; Indels 81; Gaps
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RESULT 11
PCT-US93-11298-2
; Sequence 2, Application PC/TUS9311298
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: METHOD OF CON
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US-07-989-845-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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APPLICANT: Bass, Steven
APPLICANT: Swartz, James
TITLE OF INVENTION: METH
TITLE OF INVENTION: PRODI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/989,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 75
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                               176
                                                                                                                                                                                                                                                         269 NLCDEKOKVAVEVIKNLLTNTLVLDLLGLGLTLPANKNGIA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 VSSSASVNGSVYGFPQYLCSNFLLSSPNGTQQASSLLELAQKVGYEQIVYPDVASSSSFT 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 VFGLYQQLLQSSSSAAVDIKASDLPQSGDQVNKDITQKYRTILDSTVVASQREYINS--- 216
                                                                                                                                                                                                                                                                                                                                                                                                               65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 348 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hasak, Janet E. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94080-4990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                         VKQGKPISNYYVGY----SESMCEIKDIIRDQQYNVQLIGTSD---KPYVYTDVLALNS 268
                                                                                                                                                                                                                                                                                                                                                                                                             --GGVKQIIANT----VDFGASDAPLSDEKLAQEGLFQFPTVIGGVVLAVNIPGLKSGEL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VFAEASLTGAGATFPAPVYAKWA-----DTYQK----ETGNKVNYQGI------GSS--
                                                                                                                                                                                                               -----KVNEEWKNNVGTGSTVKWPIGLG---GKGNDGIA 206
                                                                                                                                                                                                                                                                                                             VLDGKTLGDIYLGKIKKWDDEAIAKLNPGLKLPSQNIAVVRRADGSGTSFVFTSYLA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52;
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415/952-9881
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O Point San Bruno Blvd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.2%; Score 93; DB 1; Length 348; 23.5%; Pred. No. 1.2;
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     h, Inc.
METHOD OF CONTROLLING POLYPEPTIDE PRODUCTION
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NUMBER OF SEQUENCES: 3

STREET: CITY: S

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ADDRESSEE:

Genentech,

TITLE OF INVENTION:

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US-09-204-208A-11
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                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                             Sequence 11, Application US/09204208A Patent No. 6399320
APPLICANT: Ebenbichler, Christine
APPLICANT: Achhammer, Gunthar
APPLICANT: Ankenbauer, Waltraud
TITLE OF INVENTION: Modified DNA-Polymerase from Carboxydothermus hydrogenoformans an
TITLE OF INVENTION: use for Coupled Reverse Transcription and Polymerase Chain React
FILE REFERENCE: 4765
CURRENT APPLICATION NUMBER: US/09/204,208A
CURRENT FILING DATE: 1998-12-01
PRIOR APPLICATION NUMBER: EP/97121151.1
                                                                                                                                           APPLICANT: Markau, Ursula
APPLICANT: Ebenbichler, (
APPLICANT: Achhammer, Gu
APPLICANT: Ankenbauer, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 75
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
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MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                       176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  119
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nes 52; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --GGVKOIIANT----VDFGASDAPLSDEKLAQEGLFQFPTVIGGVVLAVNIPGLKSGEL 118
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910/371-7168
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                                                                                                                      US-09-269-861A-8
                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/269,861A
CURRENT FILING DATE: 199-11-22
PRIOR APPLICATION NUMBER: PCT/EP97/05391
PRIOR FILING DATE: 1997-10-01
PRIOR APPLICATION NUMBER: EP/98115873.0
PRIOR APPLICATION NUMBER: EP/98115873.0
PRIOR FILING DATE: 1996-10-03
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11
                                                                                                                                      SEQ ID NO 8
LENGTH: 831
TYPE: PRT
ORGANISM: Carboxydothermus hydrogenoformans
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Best Local
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APPLICANT:
APPLICANT:
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                                                                                 Query Match
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APPLICANT:
APPLICANT:
                                                  Matches
                                                                                                                                                                                                                                                                                                                                              APPLICANT: BONCH-OSMOLOVSKAYA, Elizaveta
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASE
FILE REFERENCE: 4494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ankenbauer, Waltraud
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                                               / Match 5.1%; Score 92.5; DB 4; Local Similarity 19.5%; Pred. No. 5.1; res 67; Conservative 52; Mismatches 110;
            21 ENGNEVKLINLIKDVLPTQVSGYNIEYTEFDCYSDASL-----QSLPDV-----FST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DS----IFLPYLVSLGGVKSLDE-------SLVRGVTGDLHSFVSSSASVNGSV 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
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Ebenbichler, Christine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Markau, Ursula
Svetlichny, Vitaly
Schmitz-Agheguian,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reiser, Astrid
                                                                                                                                                                                                                                                                                                                                                                                                          Laue, Frank
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19.5%; Pred. No. 3.
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                                                                                   Length 831;
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                                                      Indels 115;
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US-08-639-501-2
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APPLICANT: Tavtig
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APPLICANT:
                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/585,391
FILING DATE: 11-JAN-1996
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ITEM PC COMPUTER: DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                               TELEPHONE: 202-962-4810
                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 20-DEC-PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Chromosome 13-1
TITLE OF INVENTION: Susceptibility
NUMBER OF SEQUENCES: 124
                                                                                                                        APPLICATION NUMBER: US 08/573,779
FILING DATE: 18-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                          FILING DATE: 21-DEC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                       NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/639,501
FILING DATE: 29-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington
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                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 0: FILING DATE: 21-DEC-1995
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FOR SEQ ID NO:
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1201 New York Avenue N.W., Suite 1001
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Weber, Barbara
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Kamb, Alexander
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20-DEC-1995
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RESULT 15
US-08-603-753D-4
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Best Local
             COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 80.

COMPUTER: IBM PC/XT/AT compatible

OPERATING SYSTEM: Windows 3.1

SOFTWARE: WORD PERFECT 6.1 and ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/603,753D
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TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                              APPLICANT: THOMPSON, MARILYN E.
TITLE OF INVENTION: CHARACTERIZED BRCA1
TITLE OF INVENTION: PROTEINS AND SCREEN:
TITLE OF INVENTION: CHARACTERIZED BRCA1
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LENGTH: 3418 amino aci
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                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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                                                                                                                                                ZIP: 27707
                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                        CITY:
FILING DATE:
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: NORTH CAROLINA
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                                                                                                                                                                                                                      E: ARLES A. TAYLOR, JR.
SUITE 1401, UNIVERSITY TOWER,
BOULEVARD
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THOMPSON, MARILYN E.
VENTION: CHARACTERIZED BRCA1 AND BRCA2
VENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS BASED ON
VENTION: PROTEINS AND SCREENING AND BRCA2 PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                          JETTON, THOMAS L.
ROBINSON-BENION, CHERYL L.
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KING, MARY-CLAIRE
SZABO, CSILLA I.
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 20 FEB 1996
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21.7%; Pred. No. 49;
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SEQUENCE CHARACTERISTICS:
LENGTH: 3418
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t Local Similarity
ches 86; Conserv
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HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
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NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 1242/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S.
FILING DATE: 17 JAN 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUBLICATION INFORMATION:
AUTHORS: Wooster, R. et al.
TITLE: Identification of the breast cancer
TITLE: susceptability gene BRCA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: BRCA2 protein
LOCATION: 1 to 3418; Genbank locus HSU43746
IDENTIFICATION METHOD:
271 --CDEKQ-KVAVEVIKN------LLTNTLVLDLLGIGLTLPANKNGIAHLAKSSNFY--- 318
                                                                                                                                                                                                                                            439
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STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANELLE:
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DEVELOPMENTAL STAGE: adult
TISSUE TYPE: female breast
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                                                                                                 KQAISGTSPVASSFQGIKKSIFRIRESPK-ETFNASFSGHMTDPNFKKETEASESGLEIH 543
                                                                                                                                                                   KQG----KPISNYYVGYSESMCEIKDIIRDQQYNVQLIGTSDKPYVYTDVLALNSNL---
                                                                                                                                                                                                                                                                                                       FTVFGLYQQLLQSSSSAAVDIKASDLPQSGDQVNKDITQKYRTILDSTVVASQREYINSV 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RKKIF-----HEANADECEKSKNOVKEKYSFVSEVEPNDTDPLDSNVAHOKPFESGS 380
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domain at amino acids 3334-3344
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Db 544 TVCSQKEDSLCPNLIDNGSWPATTTQNSVALKNAGLISTLKKKTNKFIYAIHDETFYKGK 603

OY 319 -----AQLSQQFDAKESEVRVLRCVDFANKE 344

Search completed: January 24, 2003, 19:43:37 Job time : 25 secs

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604

KIPKDQKSELINCSAQFEANAFEAP----LTFANAD 635

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Post-processing: Minimum Match 0%
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seq length: 2000000000
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1: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being priand is derived by analysis of the total score distribution. being printed,

10987654221	Result
139.5 138.5 105.5 104.5 104.5 103.5 103.5 103.5	Score
	Query Match Length DB
10182 5024 511 511 512 512 753 761 397 4643 286	Length
22232119922	DB
ABP38314 AAG82935 AAP81161 AAP81180 AAR07574 ABP29819 ABP27624 ABP39259 ABB71609 ABB71609 ABB53627	SUMMARIES
Staphylococcus epi S. epidermidis ope Recombinant alpha- Sequence of alpha- Alpha-amylase enco Streptococcus poly Streptococcus poly Staphylococcus epi Drosophila melanog Lactococcus lactis	Description

Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections -

N-PSDB; ABN90859.

ů	4 1	4	42	41	40	39	38	37	36	ω 5	ω 4	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18							
9	•	96.5	97	97	97	97	97	97	97	97	97.5	97.5	97.5	97.5	97.5	98	98	98	98.5	98.5	98.5	98.5	98.5	98.5	98.5	99	99.5	100	100.5	100.5	101	101.5	101.5	101.5
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۷.	2 6	21	22	22	22	21	21	22	23	23	17	20	21	23	19	21	21	21	22	20	20	20	23	15	14	23	23	15	21	19	15	23	22	23
ABB498/3	ABB913/3	AAY79305	AAB30804	AAB70158	AAB65201	AAY66678	AAB24068	AAG81291	AAU96176	ABG64816	AAR99850	AAY04733	AAY53753	ABP40816	AAW68204	AAG35738	AAG35739	AAG35740	ABB71118	AAY04732	AAY04730	AAY04734	ABB53312	AAR51692	AAR32354	ABB92551	ABB90898	AAR60651	AAY78362	AAW73024	AAR60654	ABB49791	18	ABB90996
птвсекта шолосугод	Herbicidally activ	Plasmodium faicipa	Amino acid sequenc	DNA encoding human	Human PRO1009 (UNQ	Membrane-bound pro	Human PRO1009 prot		Human secreted pro	Human albumin fusi	Human type 3 inosi	Protein containing	Amino acid sequenc	phylococcus e	M. catarrhalis str	Zea mays protein f	Zea mays protein f	Zea mays protein f		Protein containing	Protein containing	Protein containing	Lactococcus lactis	B.thuringiensis se	Coleoptera toxin f		icidally			Helicobacter pylor		Listeria monocytog	Drosophila melanog	Herbicidally activ

ALIGNMENTS

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RESULT 1
ARB53814
ID ARB53
XX ARB53
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XX Stap
XX US63
PN US63
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X
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08-NOV-1997;
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97US-064964P.
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N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                         S. epidermidis open reading frame protein sequence SEQ ID NO:2964
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USPTO web site.
                                                                                                                        Staphylococcus epidermidis SR1 vaccination; endocarditis.
                                                      WO200134809-A2
                                                                                     Staphylococcus epidermidis
                                                                                                                                                                                                                03-SEP-2001
                                                                                                                                                                                                                                                                                   AAG82935 standard; Protein; 5024 AA
                    17-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGLTLPANK----NGIAHLAKSSNFYAQLSQQFDAKESEVRVL------RCVDF--
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                                                                                                                                          strain;
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                                                                                                                                          infection; diagnosis;
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CRAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. CC (II) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the CC s. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be CC used to vaccinate subjects and to raise antibodies against the bacteria. CC The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to CC AAH55090 represent specifically claimed S. epidermidis genomic DNA CC polypucleotide sequences from the present invention. AAH55091 to CC AAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention. AAH55091 to CC AAH55098 represent invention specifically claims all the polypucleotide sequences given in the sequence listing of the present specification, CC however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, con sequences are present for SEQ ID NO:4465.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-316495/33.
N-PSDB; AAH53785.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 18; Page 779-781; 2188pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 NEVKLINLIKDVĻPTQVSGYNIEYTEFDCYSDASLQSLPDVFSTDSIFLPYLVSLGGVKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
---ANKEVKNCAGVL 352
                                                                                                                                                                       DQQYNVQLIGTSDKPYVYTDVLALNSNLCDEK-----QKVAVEVIKNLLTNTLVLDLLG 296
                                                                                                                                                                                                                  L----DNAMKDLRDTLES--NSTSVPNSVNYINADK-----NLQIEFDEAL-----
                                                                                                                                                                                                                                                     LPQSGDQVNKDITQKYRTILDSTVVASQREYINSVKQGKPISNYYVGYSESMCEIKDIIR 242
                                                                                                                                                                                                                                                                                            EDTKDALNGIQRLSKAKAKAIQYVQSLSYINDAQRHIAESNIHNSDDLSSLANTLSKASD
                                                                                                                                                                                                                                                                                                                                   SSSSFTVFGLYQ-----
                                                                                                                                                                                                                                                                                                                                                                       NNQAFPVQASSNYINSDEDLKQQFDHALSNARKVLAKENGKNLDEIQIEGLKQVI-----
                                                                                                                                                                                                                                                                                                                                                                                                              --YGFPQYLCSNFLLSSPNGTQQASSLLELAQKV-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTAAKSKAEKLIDSLKFINKAQFTHANDEIMNTNSIAQLSRIVNQAFDLNDAMKSLRDEL 4031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NFTQAINNARDAL-NKTQGQNLDFNAIDTFKD-----DIFKTKD-----ALNGIER 3971
                                                       AQLEDVTNKVNSANTLTELSQLTQSTLKLNDKMKLLRDKLKTLVNPVKASLNYRNADYNL
                                                                                              LGLTLPANK----NGIAHLAKSSNFYAQLSQQFDAKESEVRVL---
                                                                                                                                    -QQASATSSKTSENPATIEEVLGLSQAIYDTKNALNGEQRLATEKSKDLKLIKGLKDLNK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5024 AA;
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Pred. No. 0.075; 
9; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DESLVRGVTGDLHSFVSSSASVNGSV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140;
                                                                                                                                                                                                                                                                                                                                         ----SSSAAVDIKASD
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                                                                                                    ----RCVDF--
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                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                  The sequence encoding the protein can be used to construct an expression vector for the prodn. of alpha amylase in yeast cells. The transformants and recombinant enzyme produced can be used in fermentation processes e.g in baking and brewing. The transformed yeasts are esp. suitable for prodn. of low carbohydrate beers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prodn. of amylolytic enzymes comprises use of recombinant having DNA from donor yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strasser A,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; ; p; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-AUG-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schwanniomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alpha amylase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant alpha-amylase.
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                                                                                                                                                                                                                                                                    18 SWNENGNEVKLINLIKDVLPTQ------VSGYNIEYTEFDCYSDASLQSLPDVFST 67
                                                                                                                                                                                                                                                                                                           Local Similarity
                                             YYELISKLNQIRNQAIKKDSAYST-YKSSVVSSSDHYIATRKGSDANQLISIFNNLGSNG
                                                                                                                                                                   C-----SNFLLSSP-----NGTQQASSLLELAQKV------GYE 145
SQDITVSN--TGYS-SGDKVIDIISCNSVLAGDSGSLSVSISGRMPQVYAPSSVLS-GSG
                                                                                                                      QIVYPDVASSS-----FTVFG----LY---QQLLQSSSSAA--
                                                                                                                                             CPYQNYMKGVTNYPLYYPVYRFFSDTSATSS--ELTSMISTLQSSCSDVSLLGNFIENHD
                                                                                                                                                                                              DNEVIGVFQTWVSDFVQNYSIDGLRIDSAKHVDTASLTKFEDASGVYNLGEVYQGDPTYT
                                                                                                                                                                                                                      DS----IFLPYLVSLGGVKSLD----ESLVRGVTGDLHSFVSSSASVN-GSVY-GFPQYL 117
                                                                                                                                                                                                                                              AWNGDGSSVD----YSSFTPFNQQSYFHDYCLITNYNDQTNVEDCWEGDTEVSLPDLSTE 214
                      -QGKPISNYYVGYSESMCEIKDIIR------DQQYNVQLIGTSDKPYVYTDVLALNSN
                                                                       ASDLPQSGDQVNKDITQK----YRTILDSTVVASQREYINSVK----
                                                                                              QVRFPSVTSDTSLIKNDMAFIILGDGIPIIYYGQEQGLNGGSDPANREALWLSGYNTDSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1988-057532/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                                               511 AA;
                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Martens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86EP-0111586
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                                                                                                                                                                                                                                                                                                          5.9%;
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                                                                                                                                                                                                                                                                                           48;
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                                                                                                                                                                                                                                                                                                          Score 105.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 by transformed microorganisms
DNA technology to give transformer
                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                       511;
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RESULT 4
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                                                                                                                                                                                                                       Query Match
Best Local S
Matches 83
                                                                                                                                                                                                                                                                                      A cosmid library is constructed from genomic DNA of ATCC26076 and this screened for inserts contg. the AA gene by ability to transform S.cerevisiae GRF 18 to histidine prototrophy. One positive cosmid (32kb; pYc1) was digested with EcoRI, religated and used to transform E.coli JA221. Positive transformants contain pYc1-alpha, which includes a 5kb EcoRI fragment contg. the gene in AAN81525.
                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                               Polypeptide prodn. esp. coding alpha a starch to ethanol
                                                                                                                                                                                                                                                                                                                                                                        Claim 18; Fig 2A-2C; 74pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1988-078794/12.
N-PSDB; AAN81525.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JUL-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence of alpha-amylase castellii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAP81180 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-1988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HETB ) HEINEKEN TEC BEHEER NV
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                                                                                                                                                   89
                                                                                                                                                                                               18 SWNENGNEVKLINLIKDVLPTQ------VSGYNIEYTEFDCYSDASLQSLPDVFST 67
                                                                                                                                                                                                                                  Local Similarity
ASDLPQSGDQVNKDITQK---YRTILDSTVVASQREYINSVK---
                                 OVRFPSVTSDTSLIKNDMAFIILGDGIPIIYYGQEQGLNGGSDPANREALWLSGYNTDSE 392
                                                                                                                                                                        AWNGDGSSVD----YSSFTPFNQQSYFHDYCLITNYNDQTNVEDCWEGDTEVSLPDLSTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ICNO
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                                                         QIVYPDVASSS-----
                                                                               CPYQNYMKGVTNYPLYYPVYRFFSDTSATSS--ELTSMISTLQSSCSDVSLLGNFIENHD 332
                                                                                                   C-----SNFLLSSP-----NGTQQASSLLELAQKV------GYE 145
                                                                                                                             DNEVIGVFQTWVSDFVQNYSIDGLRIDSAKHVDTASLTKFEDASGVYNLGEVYQGDPTYT 274
                                                                                                                                                 DS----IFLPYLVSLGGVKSLD----ESLVRGVTGDLHSFVSSSASVN-GSVY-GFPQYL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            beer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            511
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                                                                                                                                                                                                                                                                   511 AA;
                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87EP-0110370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     castellii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           breadmaking;
                                                                                                                                                                                                                                                                                                                                                                                                           amylase
                                                                                                                                                                                                                                                                                                                                                                                                                      from
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                                                                                                                                                                                                                                5.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                         cells transformed with yeast DNA se or glucoamylase, able to conve
                                                        FTVFG----LY---QLLQSSSSAA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dohmen
                                                                                                                                                                                                                     44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             biomass
                                                                                                                                                                                                                                Score 104.5;
Pred. No. 2.3;
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                                                                                                                 The expression cassette may contain a regulon (R), a signal peptide sequence (S), a foreign protein sequence (F) and a terminator (T) of which R and/or S and/or T are derived from the alpha-amylase gene of S. occidentalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR07574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schwanniomyces occidentalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                marker gene; regulon; 819
autonomously replicating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schwanniomyces yeast cells; expression cassette; alpha-amylase;
                                                                                                                                                                                                     Transformed Schwanniomyces yeast cells - cassette contg. regulon, DNA coding for
                                                                                                                                                                                                                                                                                                                                                                               EP394538-A.
                                                                                                                                                                                                                                                                                                                                                                                                              Disulfide-bond
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                                                            S contains all or part of one of the sequences represented in AAQ06383-87.
F is e.g. a cellulase, interleukin, insulin-like-growth fa
                                                                                                                                                                       Disclosure; Fig 1B(1-6); 59pp; English
                                                                                                                                                                                                                                       N-PSDB; AAQ06388
                                                                                                                                                                                                                                                 WPI; 1990-328670/44.
                                                                                                                                                                                                                                                                                                               28-APR-1989;
                                                                                                                                                                                                                                                                                                                                    28-APR-1989;
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 See
                                                                                                                                                                                                                                                                      Hollenberg C,
                                                                                                                                                                                                                                                                                           (RHEI ) RHEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lpha-amylase encoded
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           cassette
                    (bp 1537-1740).
AMY1 acts as selective
                              interferon etc.
T is pref. all or part
(bp 1537-1740)
                                                                                                        is pref. a 1.8
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                                                                                                        kb BglII-XhoI fragment (bases
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24-NOV-2000; 2000GB-0028727
07-MAR-2001; 2001GB-0005640
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New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and
                                                                                                                                                                                                                                                                                                                                                                                      29-OCT-2001; 2001WO-GB04789
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                                                                          WPI; 2002-352536/38
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Tettelin H;
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Pred. No. 2.3;
48; Mismatches
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity
                                                                                                                                                                                             Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
27-OCT-2000; 2000GB-0026333
24-NOV-2000; 2000GB-0028727
                                                                                                                                                                                                                                                                      Streptococcus polypeptide SEQ ID NO 4424.
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                                                      29-OCT-2001; 2001WO-GB04789
                                                                                                                                                             Streptococcus agalactiae
                                                                                                                                                                                                                                                                                                          02-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                 ABP27624 standard; Protein; 761
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Pred. No. 4.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus by Ogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agglactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to detect Streptococcus in a biological sample. (I) is used to detect acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity of treated may be meningitis. Nucleic streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used for affinity immunoassays, and distinguishing/identifying
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Matches
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Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
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N-PSDB; ABN68255.
                                   Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4104.
                                                                        24-JUL-2002
                                                                                                            ABP39259;
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                                                                                                                                             ABP39259
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                                                                                                                                                                                                                                                                                                                                          PYVYTDVLALNSN-LCDEKOKVAVEVIKNLLTNTLVLDLLGLGLTLPANKNGIAHLAKSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QLLQSSSSAAVDIKAS-----DLPQSGD------
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Pred. No. 4.5;
46; Mismatches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed appecification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated nucleic acid encoding a polypeptide, useful for diagnosing and
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08-NOV-1997;
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                                                                                                                                                  FYAQLSQQFDAKESEVRVLRCVDFANKEVKNCAGVLRPF 355
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                                                                                              -VSELAKRIDLTTQHYNELDHI----IENSKDTLKQF
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Pred. No. 1.9;
72; Mismatches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotesidating the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 41619; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PEKE )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2001; 2001WO-US09231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
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                                                SQRE-YINSVKQGKPISNYYVGYSESMCEIKDIIR-----
                                                                                                   LNVSVSDGKFHVFSI----
                                                                                                                                                                                                    GAFIGKVHASDQDKYDELNFSLVSGPDDMYQSSKLFNISNNTGK---IYAISNLDIGLYK 3676
                                                                                                                                                                                                                                               ASVNGSVYGFPQ--YLCSNF-LLSSPNGTQQASSLLELAQKVGYEQIVYP----DV----
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                                                                                                                                                                                                                                                                                                                                                  ---CYSDASLQSLPDVFSTDSIFLPYLVSLGGVKSLDESLVRGVTGDLHSFVSS----S
                                                                                                                                                 ----ASSSSFTVFGLYQQLLQSSSSAAVDIKASDLPQSGDQVNKDITQKYRTILDSTVVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 103.5;
Pred. No. 70;
50; Mismatches
-NIMRCRQKDVILITLQSDYQKASQHAVGNRRARSIDS
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and c
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                                                                                                                                                                                   Query Match
Best Local :
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                                                                                                                                                                                                                                                 The present invention is related to a Lactococcus lactis nucleotide sequence (ABA99521) and related proteins (ABB53300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese.

Note: The sequence data for this patent is based on equivalent patent w0200177334 [published 18-OCT-2001] which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleotide sequence useful in lactis and related species -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3820
                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-043418/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bolotine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lactococcus lactis
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                                                                                                                                        13 FPYLPSWNE--NGNEVKLINLIKDVLPTQVSGYNIEYTEFDCYSDASLQSLPDVFSTDSI
                         QASSLLELAQKV-GYEQIVYPDVASSSSFTVFGLYQQLLQSSSSAAVDIKASDLPQSGDQ 189
TPRALDSVAAAVINYNFAISAKISEKES-----IYQEPLNEDSAQWINFIAANQSDKNNK
                                                                                                             YAYLKSWNKANNGNIVS----IGDTIITPIHLYSTKYKNVTEIPDKSTIAIPNDVTNESR 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSTCQSNKNDCVH 3832
                                                                                 FLPYLVSLGGVKSLDESLVRGVTGDLHSFVSSSASVNGSVYGFPQYLCSNFLLSSPNGTQ 130
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                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID No 329; 2504pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; Protein; 286
                                                                                                                                                                                                                              286 AA;
                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         identification or Lactococcus
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                                                                                                                                                                                                                                                                                                               particularly useful in the
                                                                                                                                                                    88;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                          (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organisms -
                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; SEQ ID NO 207; 261pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                   useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to identifying target proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tietjen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-AUG-2001; 2001WO-EP09892
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 VASQREYINSVKQGKPISNYYVG----YSESMCEIKDIIRDQQYNVQLIGTSDKPYVYTD
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                           GSVPDLRGLSNLQELNLGGNKL---GPEVVPSLASNL------ITISLKNNSFGSK 216
                                                     --YPDVASSSSFTVFGLYQQLLQSSSSAAVDIKASDLPQSGDQVNKDITQKYRTILDSTV
                                                                                 GPLPSQIIRLSSSLQSLN----
                                                                                                             GDLHSFV----
                                                                                                                                       SSPSFKILCFNGHVTELTVTGNRTVKLPGRFSSDSLF-TVLTKLSNLKTL--SLVSLGIS 120
                                                                                                                                                                                            SQAFSLTFLLFLFLLPSVSESQLISSESRTLLEIQKHLQYPPTLRSWSN--WTNF-CYLP
                                                                                                                                                                                                                      TOPKTLTVGLFPY-LPSWNEN---GNEVKLINLIKDVL---PTOVSGYNIEYTEFDCYSD
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                                                                                                                                                                                                                                                   85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Weidler
                                                                                                                                                                                                                                                                                                         747 AA;
                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                          SSSASVNGSVYGFPQYLCSNFLLSSPNGTQQASSLLELAQKVGYEQIV-
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                                                                                                                                                                                                                                                              5.6%;
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                                                                                                                                                                                                                                                   48;
                                                                                                                                                                                                                                                Score 101.5; E
Pred. No. 7.2;
48; Mismatches
                                                                                                                                                                 LQSLPDVFSTDSIFLPYLVSLGGVKSLDESLVR-GVT
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                                                                                LSSNFI--SGNIPKEISSLKNLRSLVLANNLFN 169
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ABB71182
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                                                                                                                                        Query Match
Best Local S
Matches 77
                                                                                                                                                                                                                                                                 capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                           The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila
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                                                                                                                                                                                         sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2002
                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid
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           162 GLYQQLLQSSSSAAVDIKASDLPQSGDQVNK-----DITQKYRTILDSTVVASQR-EYI 214
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                                      ASWMSEQRWAGEPEVMC
                                                            SSASVNGSVYGFPQYLCSNFLLSSPNGTQQASSLLELAQKVGYEQIVYPDVASSSSFTVF 161
                                                                                                             YNIEYTEFDC-YSDASLQSLPDVFSTDSIFLPYLVSLGGVKSLDESLVRGVTGDLHSFVS 101
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DB; ABL15285.
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                                                                                                                                                                                                                                                                                                                                                                                                       from Drosophila
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77; Conserv
-NSSLCNSKLRI-LDVSRNLLTGKL
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                                                                                                                                        Conservative
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2000US-0614150.
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22.5%;
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                                    -----TIQHKSIAQEAYK-NY-----TITTSAVC 350
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                                                                                                                                                                                                                                                                                                                                                                                                         detection reagent
for elucidating co
                                                                                                                                       46;
                                                                                                                                  Score 101.5; L
Pred. No. 8.9;
46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         elucidating cell
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                                                                                      -LRFTASTSTPKSGSKIAKR--
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                                                                                                                                        Indels
                                                                                                                                                                Length
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                                                                                                    The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, are for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P, Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-García P, Tierrez-Martinez A, Amend A, Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
monocytogenes and related organisms.
Note: The sequence data for this pat
                                 sequence and proteins encoded by it are use vaccines compositions for the treatment or
                                                  for biosynthesis and biodegradation, especially biosynthesis of Vitamis B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genomesequence and proteins encoded by it are useful in pharmaceutical and
                                                                                                                                                                                                                                                                                                                                                                             Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rose
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-OCT-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Listeria monocytogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
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                                                                                                                                                                                                                                                                                                                                              related
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                                                                                                                                                                                                                                                                                                                                                           omic sequence for Listeria monocytogenes, useful e.g. for prevention of Listeria and related bacterial infections,
                                                                                                                                                                                                                                                                                                                                                                                                                   2002-010914/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RTLLVVVLDHKQSSVRALALRALATLCCAPQAINQLGSCGGI
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                                       infections
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        regulated by the phoB protein. When phosphate levels in the surrounding medium are high the PstS gene product acts a repressor. PstS variants are molecules which have been modi
                                              The pstS gene encodes a phosphate-binding periplasmic protein that is part of the high-affinity phosphate transport system mediating phosphate uptake in certain prokaryotes such as E. coli. Gene expression is induced by phosphate starvation and positively
                                                                                                                                                                                                                                                                                                                                                                                                Phosphate; phosphate binding protein; transport; repressor; polypeptide synthesis; protein synthesis; metabolism; Escherichia coli; pstS; phoB; induction; repression.
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                                                                                                                                                            Nucleic
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                                                                                                                   Claim 1; ; 58pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 DCYSDASLQSLPDVFSTDSIFLPYLV----SLGG-----VKSLDES------LVRGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             scification, but was obtained in electronic format directly from WIPO ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TVVASQREYINSVKQGKPISNYYVGYSESMCEIKDIIRDQQYNVQL-IGTSDKPYVYTDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DVASSSSFTVFGLYQQLLQSSSSAAVDIKASDLPQSGDQVNKDITQKYRTILD-----S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGDLHSFVSSSASVNGSVY--GFPQYLCSNFLLSSPNGTQQASSLLELAQKVGYEQIVYP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRLEQGKSLNEKERNTSLEVQKSL 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAL--NSNLCDEKQKVAVEVIKNL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLLTLQSDYSNMLK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESAKKS------QDAYTAAME-KAQSL--EGDKRKKAIADANKTLVDETTKNNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AKQTETTVSKSNQAIDTMLSGGVDQY--GNKL----SEKTKSFLNSAKEL-YSQ--YQ 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DAFVDAG-SAIKDAFNKDNYALTGTVEAFKOMGGEAEKTAKKTETSGKKIKDTLKLVEST 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62;
                                                                                                                                         acids encoding E. coli PstS protein variants - of polypeptide prodn. in Enterobacteriaceae ce
                                                                                                                                                                                                                                      GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
 phosphate
                                                                                                                                                                                                             Swartz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1787 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                                                 92US-0989845
                                                                                                                                                                                                                                                                                          92US-0989845
                                                                                                                                                                                                             űŖ,
binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.6%;
23.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -TNRWADGQELTAQQKKFLQQQTTDIQTELAKQNQLYVEANL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49;
region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 101.5;
Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
and no
longer function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                             cells
            modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             not g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repressors at levels of phosphate higher than about 10 micromolar. These variants may be used so that polypeptide induction may proceed in a bacterial host cell at concentrations of phosphate in the medium that are above the starvation level. This sequence is not given in the specification but is mentioned in the claims. It
                                                                                                                           01-APR-1997;
01-APR-1997;
New isolated Helicobacter polynucleotides for the diagnosis, prevention and treatmer
                                   N-PSDB;
                                                                                           (HUMA-)
                                                                                                                                                            31-MAR-1998;
                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                                                                                                therapy
                                                                                                                                                                                                                                                                                                                                                          GHPO 1516;
                                                                                                                                                                                                                                                                                                                                                                                                         02-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                having a
                                               WPI; 1998-568251/48
                                                                                                                                                                                    08-OCT-1998
                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                          Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                              AAW73024;
                                                                                                                                                                                                         WO9843479-A1
                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW73024 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 VSSSASVNGSVYGFPQYLCSNFLLSSPNGTQQASSLLELAQKVGYEQIVYPDVASSSSFT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             given in the specification but is mentioned in the claims a variant of the sequence described in AAR51473, differinging a glycine residue at position 35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VFGLYQQLLQSSSSAAVDIKASDLPQSGDQVNKDITQKYRTILDSTVVASQREYINS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NLCDEKOKVAVEVIKNLLTNTLVLDLLGLGLTLPANKNGIA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLDGKTLGDIYLGKIKKWDDEAIAKLNPGLKLPSQNIAVVRRADGSGTSFVFTSYLA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VKQGKPISNYYVGY----SESMCEIKDIIRDQQYNVQLIGTSD----KPYVYTDVLALNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --GGVKQIIANT----VDFGASDAPLSDEKLAQEGLFQFPTVIGGVVLAVNIPGLKSGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VFAEASLTGAGAGFPAPVYAKWA-----DTYQK----ETGNKVNYQGI-----GSS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53;
                                                                                          HUMAN GENOME SCI INC
MERIEUX ORAVAX PASTE
                                   AAV07913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                    P
                                                                                                                                                                                                                                                                                                                                                          infection; gastritis; ulcer; vaccine; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          346 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KVNEEWKNNVGTGSTVKWPIGLG---GKGNDGIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                         pylori.
                                                                                                                                                                                                                                                                                                                                                                                 pylori
                                                                                                                                                                                                                                                                                                                                                                                                       (first
                                                                    Kleanthous
                                                                                                                           97US-0834666.
97US-0831310.
                                                                                                                                                            98WO-US06421
                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                               /note= "encoded by NAT"
                                                                                                                                                                                                                                                                           /label= Sig_peptide
                                                                                                                                                                                                                                                    'label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                  76
                                                                                                                                                                                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.6%;
24.0%;
                                                                                           PASTEUR MERIEUX SERUMS ET VACCINS
                                                                                                                                                                                                                                                                                                                                                                                 kDa polypeptide GHPO 1516
                                                                    Ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 101;
                                                                   Lissolo L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 2.6
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
 treatment
                                                                    Miller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
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 used to develop of Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 346;
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                                                                    Tomb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48;
           products
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CC polypeptide designated GHPO 1516. It was deduced from an isolated CC genomic DNA sequence (see AAW70913). The invention provides a family CC genomic DNA sequence (see AAW70913). The invention provides a family CC of 76 kDa Helicobacter polypeptides (see AAW73022-32), as well as a CR and the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 9; Page 90-93; 184pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infections and gastroduodenal diseases
                                                                                                                                                                                                                                   378
438 VTSNTWGAGCAYVGETISALTNSIAH-----
                                                                                                                                                                                                                                                                                                                                                    245
                                                                                                                                                                                                                                                                                                                                                                                                                                                          324 EFSQVTSMIKNAQEIIAQSKIVSENAQNQNNLDTGKPFNPYTDASFAQSM-----LKNA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 TQQASSLLELAQKVGYEQIV---YPDVASSSSFTVFGLYQQLLQSSSSAAVDIKASDLPQ 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 SASVNGSVYGFPQYLCSNFLLSSPNG------- 128
                                                                                                     287 -- TNTLVLDLLGLGLTLPANKNGIAHLAKSSNFYAQLSQQFDAKESEVRVLRCVDFANK 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212 TADINGGVYQFCK--AKNGSSSSSNGGNGSSTQTTATTTQDGVTITTTYNNNKATVKFDI 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGDQVNKDITQKYRTILDSTVVASQREYINSVKQGKPISNYY-VGYSESMCEIKDIIRDQ 244
                                                                                                                                                                                                                       QAQAEMFNISEQVKKNLEVMKNNNVNEKLAGFGKEEVMTNFVSAFLASCKDGGTLPNAG 437
                                                                                                                                                                                                                                                                                                                                        QYNVQLIGTSDKPYVYTDVLALNSNLCDE----KQKVAVEVIKNLL----- 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THRAEQLLINGAANI -- MQVLNTQCPLVRSTNNENTPGGGQPWGLSTSGNACSI ---- FQQ 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           745 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.6%; Score 100.5; DB 19;
21.1%; Pred. No. 8.8;
vative 43; Mismatches 112;
-FGTQEQQIQQAENIADTL--VNFKSR 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 81; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 745;
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completed: January 24, 2003, 19:41:47 ne : 51 secs

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